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## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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<b>(21) International Application Number:</b> PCT/EP99/05652 <b>(22) International Filing Date:</b> 4 August 1999 (04.08.99) <b>(30) Priority Data:</b> 98202634.6 4 August 1998 (04.08.98) EP <b>(71) Applicant (for all designated States except US):</b> VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE [BE/BE]; Rijnvischestraat 120, B-9052 Zwijnaarde (BE). <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> LEE, Jeong, Hee [KR/BE]; Spinnmolenplein 274 (22K), B-9000 Gent (BE). VERBRUGGEN, Nathalie [BE/BE]; Avenue des Saisons, 53, B-1050 Ixelles (BE). <b>(74) Agent:</b> DE CLERCQ, Ann; Ann De Clercq & Co. B.V.B.A., Brandstraat 100, B-9830 Sint-Martens-Latem (BE).		<b>(81) Designated States:</b> AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i>
<b>(54) Title:</b> GENES INVOLVED IN TOLERANCE TO ENVIRONMENTAL STRESS  <b>(57) Abstract</b>  The present invention relates to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress resistance in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells. The present invention further relates to an isolated polynucleic acid obtainable by such a method as listed in Table 1 as well as recombinant polynucleic acid comprising the same. The present invention further relates to an isolated polypeptide encoded by a polynucleic acid of the invention. The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into a plant cell a recombinant DNA comprising a polynucleic acid as defined which when expressed in a plant cell enhances the tolerances or induces resistance to environmental stress conditions of said plant. The present invention particularly relates to plant cells, plants or harvestable parts or propagation material thereof transformed with a recombinant polynucleic acid as defined above.		

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**Genes involved in tolerance to environmental stress**

The present invention relates to molecular biology, in particular plant  
5 molecular biology. In particular, the invention relates to improvements of crop  
productivity of useful plants. One of the major limitations of crop productivity is the  
effect of environmental stress conditions on plant growth and development. An  
important goal of molecular biology is the identification and isolation of genes that can  
provide resistance or tolerance to such stresses. For agriculture, the creation of  
10 transgenic plants containing such genes provides the potential for improving the stress  
resistance or tolerance of plants.

Drought, salt loading, and freezing are stresses that cause adverse effects on  
the growth of plants and the productivity of crops. The physiological response to these  
stresses arises out of changes in cellular gene expression. Expression of a number of  
15 genes has been demonstrated to be induced by these stresses (Zhu et al., 1997;  
Shinozaki et al., 1996; Thomashow, 1994). The products of these genes can be  
classified into two groups: those that directly protect against environmental stresses  
and those that regulate gene expression and signal transduction in the stress  
response. The first group includes proteins that likely function by protecting cells from  
20 dehydration, such as the enzymes required for biosynthesis of various  
osmoprotectants, late-embryogenesis-abundant (LEA) proteins, antifreeze proteins,  
chaperones, and detoxification enzymes (Shinozaki et al., 1997, Ingram et al., 1996,  
Bray et al., 1997). The second group of gene products includes transcription factors,  
protein kinases, and enzymes involved in phosphoinositide metabolism (Shinozaki et  
25 al., 1997). An overview of the methods known to improve stress tolerance in plants is  
also given in Holmberg & Bülow, (1998).

Further studies are definitely needed to give an insight into the mechanisms  
involved in the plant response to environmental stress conditions.

The study of plants naturally adapted to extreme desiccation has led to the  
30 hypothesis that the genetic information for tolerance to environmental stress conditions  
exists in all higher plants. In glycophytes, this information would only be expressed in  
seeds and pollen grains which undergo a desiccation process.

The induction of osmotolerance in plants is very important to crop productivity:  
30 to 50 % of the land under irrigation is presently affected by salinity. Several lines of  
35 evidence also demonstrate that even mild environmental stress conditions throughout  
the growth season have a negative impact on plant growth and crop productivity. It is

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for instance known that even minor limitations in water availability cause a reduced photosynthetic rate. Unpredictable rainfall, increase in soil salinity at the beginning and the end of the growing season often result in decreased plant growth and crop productivity. These environmental factors share at least one element of stress and that is water deficit or dehydration. Drought is a significant problem in agriculture today. Over the last 40 years, for example, drought accounted for 74% of the total US crop losses of corn. To sustain productivity under adverse environmental conditions, it is important to provide crops with a genetic basis for coping with water deficit, for example by breeding water retention and tolerance mechanisms into crops so that they can grow and yield under these adverse conditions.

It is an aim of the present invention to provide a new method for screening for plant genes involved in tolerance or resistance to environmental stress.

It is an aim of the present invention to provide new plant genes, more particularly plant genes providing the potential of improving the tolerance to environmental stress conditions in plants.

It is also an aim of the present invention to provide polypeptides encoded by said new plant genes.

It is further an aim of the present invention to provide methods for producing plants with enhanced tolerance or resistance to environmental stress conditions based on said new genes.

It is also an aim of the present invention to provide recombinant polynucleic acids comprising said new genes.

It is further an aim of the present invention to provide plant cells and plants transformed with said new genes.

It is further an aim of the present invention to provide plant cells and plants with enhanced tolerance or resistance to environmental stress conditions.

The present invention relates more particularly to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

It has been found that the transfer of genes from plants which are often difficult to assay for certain characteristics, to lower eukaryotes, such as yeasts and fungi, but

in particular yeast, especially *Saccharomyces*, is relatively easy to achieve, whereby it has now been shown that the results of testing for tolerance or resistance to environmental conditions in the resulting yeast cells gives a relatively reliable measure of the capability of the inserted coding sequence or gene to induce tolerance or resistance to environmental stress in plants. Thus the expression of polynucleic acid sequences comprising the gene or coding sequence which are responsible for inducing tolerance or resistance to environmental stress conditions can be enhanced in the plant species from which it originates or in any other plant species.

In the present context the term "enhancing" must be understood to mean that the levels of molecules correlated with stress protection in a transformed plant cell, plant tissue or plant part will be "substantially increased" or "elevated" meaning that this level will be greater than the levels in an untransformed plant.

This may be achieved by inducing overexpression of suitable genetic information which is already present, or by any other suitable means of introducing into the plant cell heterologous information resulting in a capability to tolerate or resist environmental stress.

The term "environmental stress" has been defined in different ways in the prior art and largely overlaps with the term "osmotic stress". Holmberg et al., 1998 for instance define different environmental stress factors which result in abiotic stress. Salinity, drought, heat, chilling and freezing are all described as examples of conditions which induce osmotic stress. The term "environmental stress" as used in the present invention refers to any adverse effect on metabolism, growth or viability of the cell, tissue, seed, organ or whole plant which is produced by a non-living or non-biological environmental stressor. More particularly, it also encompasses environmental factors such as water stress (flooding, drought, dehydration), anaerobic (low level of oxygen, CO<sub>2</sub> etc.), aerobic stress, osmotic stress, salt stress, temperature stress (hot/heat, cold, freezing, frost) or nutrients/pollutants stress.

The term "anaerobic stress" means any reduction in oxygen levels sufficient to produce a stress as hereinbefore defined, including hypoxia and anoxia.

The term "flooding stress" refers to any stress which is associated with or induced by prolonged or transient immersion of a plant, plant part, tissue or isolated cell in a liquid medium such as occurs during monsoon, wet season, flash flooding or excessive irrigation of plants, etc.

"Cold stress" and "heat stress" are stresses induced by temperatures which are respectively, below or above, the optimum range of growth temperatures for a

particular plant species. Such optimum growth temperature ranges are readily determined or known to those skilled in the art.

“Dehydration stress” is any stress which is associated with or induced by the loss of water, reduced turgor or reduced water content of a cell, tissue, organ or whole  
5 plant.

“Drought stress” refers to any stress which is induced by or associated with the deprivation of water or reduced supply of water to a cell, tissue, organ or organism.

“Oxidative stress” refers to any stress which increases the intracellular level of reactive oxygen species.

10 The terms “salinity-induced stress”, “salt-stress” or similar term refer to any stress which is associated with or induced by elevated concentrations of salt and which result in a perturbation in the osmotic potential of the intracellular or extracellular environment of a cell.

Said salt can be for example, water soluble inorganic salts such as sodium  
15 sulfate, magnesium sulfate, calcium sulfate, sodium chloride, magnesium chloride, calcium chloride, potassium chloride etc., salts of agricultural fertilizers and salts associated with alkaline or acid soil conditions.

The transgenic plants obtained in accordance with the method of the present invention, upon the presence of the polynucleic acid and/or regulatory sequence  
20 introduced into said plant, attain resistance, tolerance or improved tolerance or resistance against environmental stress which the corresponding wild-type plant was susceptible to.

The terms “tolerance” and “resistance” cover the range of protection from a delay to complete inhibition of alteration in cellular metabolism, reduced cell growth  
25 and/or cell death caused by the environmental stress conditions defined herein before. Preferably, the transgenic plant obtained in accordance with the method of the present invention is tolerant or resistant to environmental stress conditions in the sense that said plant is capable of growing substantially normal under environmental conditions where the corresponding wild-type plant shows reduced growth, metabolism, viability,  
30 productivity and/or male or female sterility. Methodologies to determine plant growth or response to stress include, but are not limited to height measurements, leaf area, plant water relations, ability to flower, ability to generate progeny and yield or any other methodology known to those skilled in the art.

The terms “tolerance” and “resistance” may be used interchangeably in the  
35 present invention.

The methods according to the invention as set out below can be applied to any, higher plant, preferably important crops, preferably to all cells of a plant leading to an enhanced osmotic or any other form of environmental stress tolerance. By means of the embodiments as set out below, it now becomes possible to grow crops with improved yield, growth, development and productivity under environmental stress conditions, it may even become possible for instance to grow crops in areas where they cannot grow without the induced osmotolerance according to the invention.

In order to do a thorough screening for relevant plant genes and/or coding sequences, it is preferred to apply a method according to the invention whereby said cDNA library comprises copies of essentially all mRNA of said plant cell. Probably only coding sequences are sufficient. For the screening of genes involved in environmental stress, it is preferred to use a cDNA library from siliques (fruits, containing the maturing seeds), such as the siliques from *Arabidopsis*, because genes involved in for instance osmotolerance are preferentially expressed in these organs.

Although the genetic information may be introduced into yeast for screening by any suitable method, as long as it is in a functional format long enough for testing of tolerance or resistance to environmental stress conditions, it is preferred for ease of operation to use a well known vector such as a 2 $\mu$  plasmid. It is to be preferred to have the coding sequence or the gene under control of a strong constitutive yeast promoter, to enhance good expression of the gene or coding sequence of interest. Strong constitutive yeast promoters are well known in the art and include, but are not limited to the yeast TPI promoter.

The term "gene" as used herein refers to any DNA sequence comprising several operably linked DNA fragments such as a promoter and a 5' untranslated region (the 5'UTR), a coding region (which may or may not code for a protein), and an untranslated 3' region (3'UTR) comprising a polyadenylation site. Typically in plant cells, the 5'UTR, the coding region and the 3'UTR (together referred to as the transcribed DNA region) are transcribed into an RNA which, in the case of a protein encoding gene, is translated into a protein. A gene may include additional DNA fragments such as, for example, introns. As used herein, a genetic locus is the position of a given gene in the genome of a plant.

The present invention more particularly relates to an isolated polynucleic acid obtainable by a method comprising the preparation of a cDNA as set out above comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an

enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

The term "polynucleic acid" refers to DNA or RNA, or amplified versions thereof, or the complement thereof.

5       The present invention more particularly provides an isolated polynucleic acid obtainable by a method as defined above which encodes a polypeptide as listed in Table 1.

10       The capacity of an isolated polynucleic acid to confer tolerance or resistance to environmental stress conditions can be tested according to methods well-known in the art, see for example, Grillo et al. (1996), Peassarakli et al. (Editor), Nilsen et al. (1996), Shinozaki et al. (1999), Jones et al. (1989), Fowden et al. (1993) or as described in the appended examples.

15       The present invention more particularly relates to an isolated polynucleic acid which encodes a homolog of any of the polypeptides as listed in Table 1, which is chosen from:

- (a) any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, or 121, or the complementary strands thereof;
- 20       (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b), or,
- 25       (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

30       Said fragment as defined above are preferably unique fragments of said sequences.

The term "hybridizing" refers to hybridization conditions as described in Sambrook (1989), preferably specific or stringent hybridization conditions are aimed at.



Stringent conditions are sequence dependent and will be different in different circumstances. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T<sub>m</sub>) for the specific sequence at a defined ionic strength and pH. The T<sub>m</sub> is the temperature (under defined ionic strength and pH) at which  
5 50% of the target sequence hybridizes to a perfectly matched probe. Typically, stringent conditions will be those in which the salt concentration is about 0.02 molar at pH 7 and the temperature is at least about 60°C.

In the present invention, genomic DNA or cDNA comprising the polynucleic acids of the invention can be identified in standard Southern blots under stringent  
10 conditions using the cDNA sequence shown. The preparation of both genomic and cDNA libraries is within the skill of the art. Examples of hybridization conditions are also given in the Examples section.

The present invention also relates to the isolated polynucleic acids which encode polypeptides which are a homolog of the polypeptides as set out in Table 1  
15 useful for the production of plants which are resistant or tolerant to environmental stress conditions.

The present invention also relates to a polynucleic acid comprising at least part of any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121, or  
20 at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121. Preferably, said gene encodes a protein having  
25 substantially the same biological activity as the protein having the sequence of SEQ ID NO 2, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76 or 78. Said part of said gene is preferably a unique part.

The present invention preferably relates to the use of a polynucleic acid  
30 comprising at least part of any of SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%,  
35 80% or 85% identical, and most preferably at least 90% or 95% identical to any of



SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121 for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

Preferably, said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Said part of said gene is preferably a unique part.

The present invention particularly relates to an isolated polynucleic acid as defined above, which encodes a plant homolog of yeast DBF2 kinase, more particularly a DBF2 kinase homolog from *Arabidopsis thaliana* termed At-DBF2, which can at least be used to confer enhanced environmental stress tolerance or resistance in plants and yeast.

More preferably, the present invention relates to an isolated polynucleic acid encoding a plant DBF2 kinase, which is chosen from:

- (a) SEQ ID NO 1, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b), or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

Alternatively, the present invention relates to a polynucleic acid derived from a plant comprising at least part of SEQ ID NO 1, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 1. Preferably said gene encodes a protein

having substantially the same biological activity as the protein having the sequence of SEQ ID NO 2.

The present invention also relates to the use of an isolated polynucleic acid as defined above which encodes a plant HSP 17.6A protein for the production of transgenic plants, more particularly a homolog from *Arabidopsis thaliana*, which at least can be used to confer enhanced environmental stress tolerance in plants and yeast.

More preferably, the present invention relates to the use of an isolated polynucleic acid as defined above which is chosen from:

- 10 (a) SEQ ID NO 3, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- 15 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

The present invention also relates to the use of a polynucleic acid comprising at least part of SEQ ID NO 3, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 3. Preferably said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 4, for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

More preferably, the present invention relates to the use of an isolated polynucleic acid as defined above which is chosen from:

- 35 (a) any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or the complementary strand thereof;

- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

5  
10 for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

The present invention preferably relates to the use of a polynucleic acid comprising at least part of any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more  
15 preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

Preferably, said gene encodes a protein having substantially the same  
20 biological activity as the protein having the sequence of SEQ ID NO 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Said part of said gene is preferably a unique part.

According to another preferred embodiment, the present invention relates to an isolated polynucleic acid as defined above, which encodes a protein termed c74,  
25 more particularly a plant homolog of c74, even more preferably a c74 from *Arabidopsis thaliana*, which at least can be used to confer enhanced environmental stress tolerance in plants and yeast.

More particularly, the present invention relates to an isolated polynucleic acid as defined above, which is chosen from:

30

- (a) SEQ ID NO 5, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,

(d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

The present invention also relates to a polynucleic acid comprising at least part of SEQ ID NO 5, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 5. Preferably said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 6.

Two nucleic acid sequences or polypeptides are said to be "identical" according to the present invention if the sequence of nucleotides or amino acid residues, respectively, in the two sequences is the same when aligned for maximum correspondence as described below. The term "complementary to" is used herein to mean that the complementary sequence hybridizes to all or a portion of a given polynucleotide sequence.

Sequence comparisons between two (or more) polynucleic acid or polypeptide sequences are typically performed by comparing sequences of the two sequences over a "comparison window" to identify and compare local regions of sequence similarity. A "comparison window", as used herein, refers to a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman (1981), by the homology alignment algorithm of Needleman and Wunsch (1970), by the search for similarity method of Pearson and Lipman (1988), by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by visual inspection.

"Percentage of sequence identity" is determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleic acid or polypeptide sequences in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not  
5 comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the  
10 percentage of sequence identity.

The term "substantial identity" of polynucleic acid or polypeptide sequences means that a polynucleotide sequence comprises a sequence that has at least 60%, 65%, 70% or 75% sequence identity, preferably at least 80% or 85%, more preferably at least 90% and most preferably at least 95 %, compared to a reference sequence  
15 using the programs described above (preferably BLAST) using standard parameters. One of skill will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like. Substantial identity of amino acid sequences for these purposes normally means  
20 sequence identity of at least 40%, 45%, 50% or 55% preferably at least 60%, 65%, 70%, 75%, 80% or 85% more preferably at least 90%, and most preferably at least 95%. Polypeptides which are "substantially similar" share sequences as noted above except that residue positions which are not identical may differ by conservative amino acid changes. Conservative amino acid substitutions refer to the interchangeability of  
25 residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and  
30 tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, and asparagine-glutamine.



Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other, or a third nucleic acid, under stringent conditions.

More particularly, the polynucleic acids as used herein will comprise at least part of a DNA sequence which is essentially similar, or, preferentially, essentially identical or identical to one or both of the nucleotide or amino acid sequences corresponding to SEQ ID NO 1 to 121 disclosed herein, more specifically in the nucleotide sequence encoding, or the amino-acid sequence corresponding to the "active domain" of the respective protein or polypeptide.

The polynucleic acid sequences according to the present invention can be produced by means of any nucleic acid amplification technique known in the art such as PCR or conventional chemical synthesis.

For a general overview of PCR see PCR Protocols (Innis et al. (1990)).

Polynucleotides may also be synthesized by well-known techniques as described in the technical literature. See, e.g., Carruthers et al. (1982) and Adams et al. (1983). Double stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.

The present invention more particularly relates to an isolated polypeptide encoded by a polynucleic acid according to any of the polynucleic acids as defined above, or a functional fragment thereof.

The present invention preferably relates to an isolated polypeptide as listed in Table 1 or to an isolated polypeptide encoded by a polynucleic acid isolated as defined above. Preferably, the present invention relates to polypeptides or peptides having at least part of the sequence of any of SEQ ID NO NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Preferably, said part is a unique part and preferably includes the active domain of said polypeptide. Preferably said polypeptide is a recombinant polypeptide.

The term "isolated" distinguishes the protein or polynucleic acid according to the invention from the naturally occurring one.

The present invention also relates to a polypeptide comprising at least part of a polypeptide which is at least 50%, 55%, 60%, 65% identical, preferentially at least 70%, 75% identical, more preferably at least 80% or 85% identical, and most



preferably at least 90% or 95% identical to any of SEQ ID NO NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120.

5       The terms "polypeptide" and "protein" are used interchangeably throughout the present description.

Said polypeptide preferably has the ability to confer tolerance or resistance to environmental stress conditions in at least plants, plant parts, plant tissues, plant cells, plant calli or yeast.

10       The term "functional fragment" refers to a fragment having substantially the biological activity of the protein from which it is derived.

The polypeptides of the present invention may be produced by recombinant expression in prokaryotic and eukaryotic engineered cells such as bacteria, yeast or fungi. It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression in these systems.

15       The present invention more particularly relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising transiently introducing into a plant cell a recombinant DNA comprising any of the polynucleic acids as defined above which when (over)expressed in a plant cell enhances tolerance or resistance to environmental stress of said plant.

20       The term "plant cell" as defined above also comprises plant tissue or a plant as a whole. The present invention more particularly relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising transiently introducing into a plant cell a recombinant DNA comprising any of the polynucleic acids encoding a protein as listed in Table 1 which when (over)expressed in a plant cell enhances tolerance or resistance to environmental stress in said plant.

25       The term "(over)expression" refers to the fact that the polypeptides of the invention encoded by said polynucleic acid are preferably expressed in an amount effective to confer tolerance or resistance to the transformed plant, to an amount of salt, heat, cold, (or other stress factors) that inhibits the growth of the corresponding untransformed plant.

30       Several methods to obtain transient introduction and expression of a recombinant DNA in a plant are known to the art. For example, plant virus vectors can

be used to obtain such purpose. Examples conferring to the use of plant viral vectors are described in Porta and Lomonossoff (1996), WO9320217 and US 5,589,367.

The present invention also relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising stably  
5 introducing into the genome of a plant cell a recombinant DNA comprising any of the polynucleic acids as defined above which when (over)expressed in a plant cell enhances the environmental stress tolerance or resistance of a plant.

The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress conditions, said method  
10 comprising introducing into the genome of a plant cell a recombinant DNA comprising any of the polynucleic acids encoding a protein as listed Table 1 which when (over)expressed in a plant cell enhances the environmental stress resistance of said plant.

According to a preferred embodiment, the present invention relates to a  
15 method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding a DBF2 kinase, preferably a plant DBF2 kinase, most preferably an Arabidopsis DBF2 kinase.

According to another preferred embodiment, the present invention relates to a  
20 method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding an HSP 17.6A protein, preferably a plant HSP 17.6A protein, most preferably an Arabidopsis HSP 17.6A.

According to a preferred embodiment, the present invention relates to a  
25 method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding a c74 protein, preferably a plant c74 protein, most preferably a Arabidopsis c74 protein.

Preferably, the present invention relates to a method as defined above,  
30 comprising:

(a) introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:

- a polynucleic acid as defined above, and,
- a plant expressible promoter, whereby said  
35 polynucleic acid is in the same transcriptional unit

and under the control of said plant-expressible promoter, and,

(b) regenerating said plant from said plant cell.

The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising indirectly increasing or inducing the expression of an endogenous gene in said plant comprised within a polynucleic acid as defined above or indirectly increasing or inducing the activity of a protein as defined above.

The present invention also relates to a method as defined above, comprising:

(a) introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:

- a DNA encoding a protein which when expressed in said plant cell at an effective amount indirectly increases or induces the expression of an endogenous polynucleic acid or indirectly increases or induces the protein activity of a protein encoded by said polynucleic acid of the present invention, and,
- a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter, and,

(b) regenerating said plant from said plant cell.

A "recombinant" DNA molecule will comprise a "heterologous sequence" meaning that said recombinant DNA molecule will comprise a sequence originating from a foreign species, or, if from the same species, may be substantially modified from its original form. For example, a promoter operably linked to a structural gene which is from a species different from which the structural gene was derived, or, if from the same species, may be substantially modified from its original form.

The present invention also relates to a method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress conditions, said method comprising indirectly increasing or inducing the expression of an endogenous gene in said plant comprised within a polynucleic acid as defined above or indirectly increasing or inducing the activity of a protein of the invention as defined above. According to this embodiment, other polynucleic acids modulating the expression or the activity of a protein according to the present invention may be introduced

transiently or stably into the genome of said plants. The term "modulating" means enhancing, inducing, increasing, decreasing or inhibiting.

Increase or induction of expression or induction or increase of protein activity is required when said regulator protein is a positive regulator of the expression or the activity of at least one of the polynucleic acids or protein of the present invention.

Decrease or inhibition of expression or decrease or inhibition of protein activity is required when said regulator protein is a negative regulator of the expression or activity of at least one of the polynucleic acids or proteins of the present invention.

Increase of the activity of said polypeptide according to the present invention is obtained, according to one embodiment of the invention, by influencing endogenous gene expression in the plant. This is preferably achieved by the introduction of one or more polynucleic acid sequences according to the invention into the plant genome, in a suitable conformation for gene expression (e.g. under control of a plant-expressible promoter). This will result in increased or induced expression (overexpression) or increased or induced activity of the protein in the plant cells, and, in the presence of an adequate substrate, in an increase of tolerance or resistance to environmental stress conditions in a transgenic plant or plant cell as compared to a non-transgenic plant or plant cell. This increase in tolerance can be measured by measuring mRNA levels, or where appropriate, the level or activity of the respective protein (e.g. by means of ELISA, activity of the enzyme as measured by any technique known in the art). Endogenous gene expression refers to the expression of a protein which is naturally found in the plant, plant part or plant cell concerned.

Alternatively, said enhanced tolerance or resistance to environmental stress conditions may be achieved by introducing into the genome of the plant, one or more transgenes which interact with the expression of endogenous genes (polynucleic acids) according to the present invention, by anti-sense RNA, co-suppression or ribozyme suppression of genes which normally inhibit the expression of the polynucleic acids of the present invention or by suppression of genes which normally inhibit the activity of the polypeptides of the invention as defined above.

For inhibition of expression, the nucleic acid segment to be introduced generally will be substantially identical to at least a portion of the endogenous gene or genes to be repressed. The sequence, however, need not be perfectly identical to inhibit expression. The vectors of the present invention can be designed such that the inhibitory effect applies to other genes within a family of genes exhibiting homology or substantial homology to the target gene.

For antisense suppression, the introduced sequence also need not be full length relative to either the primary transcription product or fully processed mRNA.

Generally, higher homology can be used to compensate for the use of a shorter sequence.

5 Furthermore, the introduced sequence need not have the same intron or exon pattern, and homology of non-coding segments may be equally effective. Normally, a sequence of between about 30 or 40 nucleotides up to the full length sequence should be used, though a sequence of at least about 100 nucleotides is preferred, a sequence of at least about 200 nucleotides is more preferred, and a sequence of  
10 about 500 to about 1700 nucleotides is especially preferred.

Catalytic RNA molecules or ribozymes can also be used to inhibit expression of genes as explained above. It is possible to design ribozymes that specifically pair with virtually any target RNA and cleave the phosphodiester backbone at a specific location, thereby functionally inactivating the target RNA. In carrying out this cleavage,  
15 the ribozyme is not itself altered, and is thus capable of recycling and cleaving other molecules, making it a true enzyme. The inclusion of ribozyme sequences within antisense RNAs confers RNA-cleaving activity upon them, thereby increasing the activity of the constructs.

A number of classes of ribozymes have been identified. One class of  
20 ribozymes is derived from a number of small circular RNAs which are capable of selfcleavage and replication in plants. The RNAs replicate either alone (viroid RNAs) or with a helper virus (satellite RNAs). Examples include RNAs from avocado sunblotch viroid and the satellite RNAs from tobacco ringspot virus, lucerne transient streak virus, velvet tobacco mottle virus, solanum nodiflorum mottle virus and  
25 subterranean clover mottle virus. The design and use of target RNA-specific ribozymes is described in Haseloff et al. (1988).

Another method of suppression of gene expression is sense suppression. Introduction of nucleic acid configured in the sense orientation has been shown to be an effective means by which to block the transcription of target genes. For an example  
30 of the use of this method to modulate expression of endogenous genes see, Napoli et al. (1990), and U.S. Patents Nos. 5,034,323, 5,231,020, and 5,283,184.

The suppressive effect may occur where the introduced sequence contains no coding sequence per se, but only intron or untranslated sequences homologous to sequences present in the primary transcript of the endogenous sequence. The  
35 introduced sequence generally will be substantially identical to the endogenous



sequence intended to be repressed. This minimal identity will typically be greater than about 65%, but a higher identity might exert a more effective repression of expression of the endogenous sequences. Substantially greater identity of more than about 80% is preferred, though about 95% to absolute identity would be most preferred. As with  
5 antisense regulation, the effect should apply to any other proteins within a similar family of genes exhibiting homology or substantial homology.

For sense suppression, the introduced sequence, needing less than absolute identity, also need not be full length, relative to either the primary transcription product or fully processed mRNA. This may be preferred to avoid concurrent production of  
10 some plants which are overexpressers. A higher identity in a shorter than full length sequence compensates for a longer, less identical sequence. Furthermore, the introduced sequence need not have the same intron or exon pattern, and identity of non-coding segments will be equally effective. Normally, a sequence of the size ranges noted above for antisense regulation is used.

15 Other methods for altering or replacing genes known in the art can also be used to inhibit expression of a gene. For instance, insertional mutants using T-DNA or transposons can be generated. See, e.g., Haring et al. (1991) and Walbot (1992). Another strategy in genetic engineering of plants and animals is targeted gene replacement. Homologous recombination has typically been used for this purpose  
20 (see, Capecchi (1989)).

Alternatively, the present invention also relates to a method as defined above wherein said DNA encodes a sense or antisense RNA or a ribozyme capable of indirectly increasing or inducing the expression of an endogenous polynucleic acid sequence according to the invention as defined above or increasing or inducing the  
25 activity of a protein of the invention as defined above. Preferably said endogenous polynucleic acid encodes a protein as listed in Table 1.

The present invention also relates to a recombinant polynucleic acid comprising: a polynucleic acid as defined above, and, a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control  
30 of said plant-expressible promoter.

The present invention also relates to a recombinant polynucleic acid comprising:

(a) a DNA encoding a protein which when expressed in said plant at an effective amount indirectly increases or induces the expression of an endogenous



polynucleic acid as defined above or indirectly increases or induces the protein activity of a polypeptide as defined above, and,

(b) a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.

5 An "endogenous" polynucleic acid refers to a polynucleic acid that is already present in the plant species before transformation.

Said recombinant polynucleic acid as described here above is generally also referred to as a "recombinant vector" or an "expression cassette". An expression cassette of the invention can be cloned into an expression vector by standard  
10 methods. The expression vector can then be introduced into host cells by currently available DNA transfer methods.

The present invention also relates to the recombinant polynucleic acid as defined above, comprising a DNA which encodes an anti-sense RNA, a ribozyme or a sense RNA which increases or induces the activity of a protein as defined above in  
15 said cell. Preferably said protein is listed in Table 1.

More particularly, the present invention relates to a recombinant polynucleic acid comprising at least part of the nucleotide sequence of any of SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99,  
20 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121.

Preferably, the present invention relates to a recombinant polynucleic acid comprising at least part of the coding sequence of a gene encoding a protein as listed in Table 1. Preferably, said "part" is a unique part of any of said nucleotide sequences. (26-28) As used herein, the term a "plant-expressible promoter" refers to a promoter  
25 that is capable of driving transcription in a plant cell. This includes any promoter of plant origin, including the natural promoter of the transcribed DNA sequence, but also any promoter of non-plant origin which is capable of directing transcription in a plant cell. The promoter may also be an artificial or synthetic promoter. The term "plant-expressible promoter" includes, but is not restricted to, constitutive, inducible, organ-,  
30 tissue-specific or developmentally regulated promoters.

According to the invention, production and/or activity of a polypeptide according to the present invention in a plant or in plant parts is increased by introducing *one or more* polynucleic acids according to the invention into the genome of the plant. More specifically, the constitutive promoter can be, but is not restricted to, one of the  
35 following: a 35S promoter (Odell et al. (1985)), a 35S'3 promoter (Hull and Howell

(1987)), the promoter of the nopaline synthase gene ("PNOS") of the Ti-plasmid (Herrera -Estrella, (1983)) or the promoter of the octopine synthase gene ("POCS", De Greve et al. (1982)). It is clear that other constitutive promoters can be used to obtain similar effects. A list of plant-expressible promoters that can be used according to the present invention is given in Table 2.

For specific embodiments of this invention, the use of inducible promoters can provide certain advantages. Modulation of protein levels or protein activity may be required in certain parts of the plant, making it possible to limit modulation to a certain period of culture or developmental stage of the plant.

For specific embodiments of this invention, the use of organ- or tissue-specific or chemical inducible promoters can provide certain advantages. Thus, in specific embodiments of the invention, the gene(s) or part thereof is (are) placed under the control of a promoter directing expression in specific plant tissues or organs, such as for instance roots, leaves, harvestable parts, etc.

It is also possible to use a promoter that can be induced upon the environmental stress conditions. Such promoters can be taken for example from stress-related genes which are regulated directly by an environmental, i.e. preferable abiotic, stress in a plant cell, including genes for which expression is increased, reduced or otherwise altered. These stress related genes comprise genes the expression of which is either induced or repressed by anaerobic stress, flooding stress, cold stress, dehydration stress, drought stress, heat stress or salinity. An exemplary list of such promoters is given in Table 3.

The recombinant polynucleic acids according to the present invention may include further regulatory or other sequences from other genes, such as leader sequences (e.g. the cab22 leader from Petunia), 3' transcription termination and polyadenylation signals (e.g. from the octopine synthase gene or the nopaline synthase gene), plant translation initiation consensus sequences, introns, transcription enhancers and other regulatory elements such as adh intron 1, etc, which is or are operably linked to the gene or a fragment thereof. Additionally, the recombinant polynucleic acid can be constructed and employed to target the gene product of the polynucleic acid of the invention to a specific intracellular compartment within a plant cell on to direct a protein to the extracellular environment. This can generally be obtained by operably joining a DNA sequence encoding a transit or signal peptide to the recombinant polynucleic acid.

The recombinant DNA comprising one or more polynucleic acids according to the present invention may be accompanied by a chimeric marker gene (Hansen et al., 1999 and references therein). The chimeric marker gene can comprise a marker DNA that is operably linked at its 5' end to a plant-expressible promoter, preferably a constitutive promoter, such as the CaMV 35S promoter, or a light inducible promoter  
5 such as the promoter of the gene encoding the small subunit of Rubisco; and operably linked at its 3' end to suitable plant transcription 3' end formation and polyadenylation signals. It is expected that the choice of the marker DNA is not critical, and any suitable marker DNA can be used. For example, a marker DNA can encode a protein  
10 that provides a distinguishable color to the transformed plant cell, such as the A1 gene (Meyer et al., (1987)), can provide herbicide resistance to the transformed plant cell, such as the *bar* gene, encoding resistance to phosphinothricin (EP 0 242 246), or can provide antibiotic resistance to the transformed cells, such as the *aac(6')* gene, encoding resistance to gentamycin (WO94/01560).

15 According to another embodiment, the present invention relates to the use of the polynucleic acids above as selectable marker gene. More preferably, the present invention also relates to the use of the plant DBF2 gene as defined above as selectable marker gene, selection taking place with treatment with a stress condition.

20 The recombinant DNA vectors according to the present invention comprising the sequences from genes of the invention will typically also comprise a marker gene which confers a selectable phenotype on plant cells. For example, the marker may encode biocide resistance, particularly antibiotic resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance  
25 to chlorosulfuron or Basta.

The present invention also relates to a recombinant host cell transformed with an isolated polynucleic acid as defined above. Said host can be any host known in the art. Preferably said recombinant host cell is a plant cell, yeast, fungi, insect cell, etc. In order to be efficiently expressed in said host, said polynucleic acids can be combined  
30 with any promoter known to function in said host system. Methods for transforming said host cells are also well known in the art.

The present invention particularly also relates to a plant cell transformed with at least one recombinant polynucleic acid as defined above.

The present invention also relates to a plant consisting essentially of plant cells  
35 transformed with at least one recombinant polynucleic acid as defined above.

A "transgenic plant" refers to a plant comprising a transgene in the genome of essentially all of its cells.

DNA constructs of the invention may be introduced into the genome of the desired plant host by a variety of conventional techniques (see for example Hansen et al., 1999 for review and WO 99/05902). For example, DNA constructs of the invention may be introduced into the genome of the desired plant host by using techniques such as protoplast transformation, biolistics or microprojectile bombardment or Agrobacterium mediated transformation.

Microinjection techniques are known in the art and well described in the scientific and patent literature. The introduction of DNA constructs using polyethylene glycol precipitation is described in Paszkowski et al. (1984).

Electroporation techniques are described in Fromm et al. (1985). Biolistic transformation techniques are described in Klein et al. (1987).

Alternatively, the DNA constructs may be combined with suitable T-DNA flanking regions and introduced into a conventional Agrobacterium host vector. The virulence functions of the Agrobacterium host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria. Agrobacterium tumefaciens-mediated transformation techniques, including disarming and use of binary vectors, are well described in the scientific literature. See, for example Horsch et al. (1984), and Fraley et al. (1983).

Transformed plant cells which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the transformed genotype and thus the desired phenotype. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium. Plant regeneration from cultured protoplasts is described in Evans et al. (1983); and Binding (1985). Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee et al. (1987).

The polynucleic acids and polypeptides of the invention can be used to confer desired traits on a broad range of plants, including monocotyledonous or dicotyledonous plants, preferably they belong to a plant species of interest in agriculture, wood culture or horticulture, such as a crop plant, root plant, oil producing plant, wood producing plant, fruit producing plant, fodder or forage legume, companion or ornamental or horticultured plant. The plants can include species from the genera Actinidia, Apium, Allium, Ananas, Arachis, Arisaema, Asparagus, Atropa, Avena, Beta,

Brassica, Carica, Cichorium, Citrus, Citrullus, Capsicum, Cucumis, Cucurbita, Cydonia, Daucus, Diospyros, Fragaria, Glycine, Gossypium, Helianthus, Heterocallis, Hordeum, Hyoscyamus, Ipomoea, Lactuca, Linum, Lolium, Lycopersicon, Malus, Mangifera, Manihot, Majorana, Medicago, Musa, Nicotiana, Oryza, Panicum, Pannesetum, Persea, Petroselinum, Phaseolus, Pisum, Pyrus, Prunus, Raphanus, Rheum, Ribes, Rubus, Saccharum, Secale, Senecio, Sinapis, Solanum, Sorghum, Spinacia, Trigonella, Triticum, Vaccinium, Vitis, Vigna, Zea, and Zingiber. Additional species are not excluded. Crops grown on cultivated lands in arid and semi-arid areas in which irrigation with ground water is needed may advantageously benefit from the invention.

One of skill will recognize that after the recombinant polynucleic acid is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed. As described before, the plant cells, plant tissue, in particular, transgenic plants of the invention display a certain higher or enhanced degree of tolerance (or even resistance) to environmental stress conditions compared to the corresponding wild-type plants. For the meaning of "environmental stress", see supra. In a preferred embodiment of the present invention, the transgenic plant displays increased tolerance to osmotic stress, salt stress, cold and/or heat stress. An increase in tolerance to such environmental stress is understood to refer to a tolerance to a level of such stress which inhibits the growth and productivity of the corresponding untransformed plant, as determined by methodologies known to the art. Such increased tolerance in transgenic plants is related to an increased expression level in the transgenic plant or parts thereof of one or more of the polynucleic acids of the present invention and/or to an increased level of activity of the polypeptide(s) encoded by said polynucleic acid, as determined by methodologies known to the art. In comparison with their untransformed counterparts, and determined according to methodologies known in the art, a transgenic plant according to the present invention shows an increased growth, viability, metabolism, fertility and/or productivity under mild environmental stress conditions. In the alternative, a transgenic plant according to the invention can grow under environmental stress conditions wherein the untransformed counterparts can not grow. An increase in tolerance to salt stress is understood to refer to the capability of the transgenic plant to grow under stress conditions which inhibit the growth of at least 95% of the parent, non-stress tolerant plants from which the stress tolerant transgenic



plants are derived. Typically, the growth rate of stress tolerant plants of the invention will be inhibited by less than 50%, preferably less than 30%, and most preferably will have a growth rate which is not significantly inhibited by growth conditions which inhibit the growth of at least 95% of the parental, non-stress tolerant plants. In an alternative  
5 example, under mild environmental stress conditions, the growth and/or productivity of the transgenic plants is statistically at least 1 % higher than for their untransformed counterparts, preferably more than 5 % higher and most preferably more than 10 % higher.

Any transformed plant obtained according to the invention can be used in a  
10 conventional breeding scheme or in *in vitro* plant propagation to produce more transformed plants with the same characteristics and/or can be used to introduce the same characteristic in other varieties of the same or related species.

Furthermore, the characteristic of the transgenic plants of the present invention to maintain normal/rapid/high growth rates under environmental stress conditions can  
15 be combined with various approaches to confer environmental stress tolerance with the use of other stress tolerance genes. Some examples of such stress tolerant genes are provided in Holmberg and Bülow (1998). Most prior art approaches which include the introduction of various stress tolerance genes have the drawback that they result in reduced or abnormal growth (compared to non-transgenic controls) under normal,  
20 non-stressed conditions, namely stress tolerance comes at the expense of growth and productivity (Kasuga et al., 1999). This correlation between constitutive expression of stress-responsive genes and reduced growth rates under normal growth conditions indicates the presence of cross talk mechanisms between stress response control and growth control.

Furthermore, the characteristic of the transgenic plants of the present invention to display tolerance to environmental stress conditions can be combined with various  
25 approaches to confer to plants other stress tolerance genes, e.g., osmotic protectants such as mannitol, proline; glycine-betaine, water-channeling proteins, etc. Thus, the approach of the present invention to confer tolerance to environmental stress  
30 conditions to plants can be combined with prior art approaches which include introduction of various stress tolerance genes. Combination of these approaches may have additive and/or synergistic effects in enhancing tolerance or resistance to environmental stress.

Thus, it is immediately evident to the person skilled in the art that the method of  
35 the present invention can be employed to produce transgenic stress tolerant plant with



any further desired trait (see for review TIPTEC Plant Product & Crop Biotechnology 13 (1995), 312-397) comprising:

- (i) herbicide tolerance (DE-A 3701623; Stalker (1988)),
- (ii) insect resistance (Vaek (1987)),
- 5 (iii) virus resistance (Powell (1986), Pappu (1995), Lawson (1996)),
- (iv) ozone resistance (Van Camp (1994)),
- (v) improving the preserving of fruits (Oeller (1991)),
- (vi) improvement of starch composition and/or production (Stark (1992), Visser (1991)),
- 10 (vii) altering lipid composition (Voelker (1992)),
- (viii) production of (bio)polymers (Poirer (1992)),
- (ix) alteration of the flower color, e.g., by manipulating the anthocyanin and flavonoid biosynthetic pathway (Meyer (1987), WO90/12084),
- (x) resistance to bacteria, insects and fungi (Duering (1996), Strittmatter (1995), Estruch (1997)),
- 15 (xi) alteration of alkaloid and/or cardiac glycoside composition,
- (xii) inducing maintaining male and/or female sterility (EP-A1 0 412 006; EP-A1 0 223 399; WO93/25695);
- (xiii) higher longevity of the inflorescences/flowers, and
- 20 (xvi) stress resistance.

Thus, the present invention relates to any plant cell, plant tissue, or plant which due to genetic engineering displays an enhanced tolerance or resistance to environmental stress obtainable in accordance with the method of the present invention and comprising a further nucleic acid molecule conferring a novel phenotype to the plant such as one of those described above.

The present invention also relates to a callus or calli consisting essentially of plant cells as defined here above. Such transgenic calli can be preferably used for the production of secondary metabolites in plant cell suspension cultures.

The present invention also relates to any other harvestable part, organ or tissue or propagation material of the plant as defined here above.

The present invention also relates to the seed of a transgenic plant as defined here above, comprising said recombinant DNA.

The present invention also relates to the use of any isolated polynucleic acid as defined above to produce transgenic plants.

The present invention also relates to the use of a recombinant polynucleic acid as defined above, to produce transgenic plants, preferably transgenic plants having an enhanced tolerance or resistance to environmental stress conditions. Preferably said polynucleic acid encodes a polypeptide as listed in Table 1.

5       The present invention also relates to the use of an isolated polynucleic acid as defined above, to produce transgenic callus having an enhanced tolerance or resistance to environmental stress conditions. Preferably said polynucleic acid encodes a polypeptide as listed in Table 1.

10       The present invention also relates to probes and primers derived from the genes of the invention that are useful for instance for the isolation of additional genes having sequences which are similar to but differ from any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, but which encode a protein  
15       having substantially the same biological activity as a protein having the amino acids sequence of any of SEQ ID NO 2 to 120 (even numbers) by techniques known in the art, such as PCR. The presence of a homologous gene in another plant species can for instance be verified by means of Northern or Southern blotting experiments.

20       The present invention also relates to the cloning of the genomic counterpart of any of the cDNA sequences as represented in SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121. These genomic counterparts can be selected from a genomic library using these cDNA sequences as a probe. The present  
25       invention also relates to the coding region as well as the promoter region of any of said genomic clones.

      The term "probe" according to the present invention refers to a single-stranded oligonucleotide *sequence* which is designed to specifically hybridize to any of the polynucleic acids of the invention.

30       The term "primer" refers to a single stranded oligonucleotide sequence capable of acting as a point of initiation for synthesis of a primer extension product which is complementary to the nucleic acid strand to be copied. Preferably the primer is about 5-50 nucleotides long. The term "target region" of a probe or a primer according to the present invention is a sequence within the polynucleic acid(s) to which the probe or the  
35       primer is completely complementary or partially complementary (i.e. with some degree

of mismatch). It is to be understood that the complement of said target sequence is also a suitable target sequence in some cases.

"Specific hybridization" of a probe to a target region of the polynucleic acid(s) means that the probe forms a duplex with part of this region or with the entire region under the experimental conditions used, and that under those conditions this probe  
5 does substantially not form a duplex with other regions of the polynucleic acids present in the sample to be analysed.

"Specific hybridization" of a primer to a target region of the polynucleic acid(s) means that, during the amplification step, said primer forms a duplex with part of this  
10 region or with the entire region under the experimental conditions used, and that under those conditions the primer does not form a duplex with other regions of the polynucleic acids present in the sample to be analysed. It is to be understood that "duplex" as used hereby, means a duplex that will lead to specific amplification.

Preferably, the probes of the invention are about 5 nucleotides to about 1 Kb  
15 long, more preferably from about 10 to 25 nucleotides. The nucleotides as used in the present invention may be ribonucleotides, deoxyribonucleotides and modified nucleotides such as inosine or nucleotides containing modified groups which do not essentially alter their hybridization characteristics. The probes according to the present invention preferably include parts of the cDNA sequences of any of the polynucleic  
20 acids as defined above.

The present invention also relates to a composition comprising a polynucleic acid sequence as defined above, a polypeptide as defined above, a probe as defined above or a primer as defined above.

The present invention also relates to a pharmaceutical or agrochemical  
25 composition comprising said polynucleic acid, a polypeptide of the invention as defined above.

The present invention also relates to antibodies specifically reacting with a protein or polypeptide according to the present invention.

The following Examples describe by way of example the tolerance and/or  
30 resistance to several environmental stress conditions observed for transgenic plants and yeast overexpressing some of the polynucleic acids according to the present invention. Unless stated otherwise in the Examples, all recombinant DNA techniques are carried out according to standard protocols as described in Sambrook et al. (1989) and in volumes 1 and 2 of Ausubel et al. (1994). Standard materials and methods for  
35 plant molecular work are described in Plant Molecular Biology Labfax (1993) by R.D.D.

Croy, jointly published by BIOS Scientific Publications Ltd. (UK) and Blackwell Scientific Publications, UK.

These examples and figures are not to be construed as limiting to any of the embodiments of the present invention as set out above. All of the references  
5 mentioned herein are incorporated by reference.

## BRIEF DESCRIPTION OF THE FIGURES AND TABLES

Figure 1. *At-DBF2* encodes a functional homolog of the yeast *Dbf2* (A) Comparison of the deduced amino acid sequence of *At-DBF2* with that of yeast *DBF2*. Gaps were introduced to optimize the alignment. Roman numerals above the *At-DBF2* sequence indicate the protein kinase catalytic subdomains defined by Hanks et al. (1988). (B) Complementation of *dbf2*. The *dbf2* mutant S7-4A [*MATa dbf2Δ::URA3 ura3 leu2 ade5 trp1 his7*] (Toyn and Johnston, 1994) (B1) forms swollen pairs of daughter cells (dumbbells) at restrictive temperature (37° C). The defective morphology of the *dbf2* mutant can be complemented by transformation with the pYX112 centromeric plasmid (Ingenius, R&D system) containing the *At-DBF2* cDNA (B2) or *DBF2* (B3); wild type (CG378 strain, *MATa ade5 leu2 trp1 ura3*) (B4). Log phase cultures were shifted from 28°C to 37°C and photographed after 16 hours. After 16 hours, 98% of the S7-4A cells arrested with a dumbbell morphology (B1) whereas 6,1 and 0% of dumbbells were observed in B1, B3 and B4. Strains were kindly provided by (Dr Lindl, Max Planck Institut für Züchtungsforschung, Köln, Germany).

Figure 2. Overexpression of *DBF2* or *At-DBF2* enhances tolerance to osmotic, salt, heat and cold stress. Yeast cells were grown in YPD and cell density was adjusted to OD600 at 2. (1) DY, (2) DY transformed with pYX212 containing *DBF2*, pYX-YDBF2, (3) DY transformed with vector alone or (4) with vector containing *At-DBF2*, pYX-AtDBF2. Serial dilutions were made in step 1:10. Ten µl of each dilution was spotted on solid YPD medium (control) supplemented with 2M sorbitol (osmotic stress) or 1.2 M NaCl (salt stress) or 4µl H<sub>2</sub>O<sub>2</sub> (oxidative stress) and incubated at 28°C or at 42°C (heat stress) or at 4°C (cold stress) for 3 days.

Figure 3. *DBF2* and *At-DBF2* are induced by stress. (a) Northern analysis showing the kinetics of *At-DBF2* induction in plants treated with PEG 6000 20 % and the one of *DBF2* in yeast treated with sorbitol 2M for the time indicated. (b) Northern analysis of *At-DBF2* in 10 day-old-plants grown for 5 hours in control conditions (as described in Verbruggen et al. 1993) (1), at 37°C (2), with PEG 6000 20 % (3), NaCl 1% (4), at 4°C (5) or with 0.4 mM H<sub>2</sub>O<sub>2</sub> (6); and of *DBF2* in yeast cells grown for 11/2 hour in YPD (1), at 37°C (2), with sorbitol 2M (3), with NaCl 1.2 M (4), at 4°C (5) or with 0.4 mM H<sub>2</sub>O<sub>2</sub> (6). Control of loading has been done with EtBr staining and is shown under each Northern analysis.



(c) Western analysis of At-DBF2 in Arabidopsis. Samples are similar to those analysed in (b). Antibodies used were raised against yeast Dbf2 and kindly provided by Dr L. Leindl (Max Planck Institut für Züchtungsforschung, Köln, Germany).

5           Figure 4. *DBF2* overexpression can suppress *hog1* osmosensitivity. The *hog1* mutant (4) [W303-1A, *MATa*, *hog1Δ::TRP1*] and wild type (W303) (1) were kindly provided by Dr Thevelein (Katholieke Universiteit Leuven, Belgium). The *hog1* mutant was transformed with pYX-YDBF2 (2) or pYX-AtDBF2 (3). Each of the 4 strains was grown for 16 hours in YPD (rich medium), and cell density was adjusted to  
10   OD600 at 2. Serial dilutions, 1:10 were made at five consecutive steps. Ten microliter of each dilution was spotted on solid YPD medium (control) or solid YPD medium supplemented with 0,9 M NaCl and incubated at 28°C for 3 days.

          Figure 5. *T-DBF2* (*Nicotiana tabacum* DBF2) is periodically expressed during  
15   plant cell cycle. Tobacco *DBF2* expression has been followed in BY2 cells synchronised with aphidicolin (a & b) or with propyzamide (c & d) with *At-DBF2* as probe. The measure of relative rate of DNA synthesis and of the mitotic index, the use of the cell cycle markers *CYCB1.2* and *H4* markers have been previously described (Reicheld et al., 1995). *T-DBF2* transcript levels were quantified from the blots shown  
20   in b and d using a PhosphorImager (Molecular Dynamics).

          Figure 6. shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left  
25   section) upon applying a salt stress of 200 mM NaCl overnight.

          Figure 7 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left  
30   section) upon applying an osmotic stress induced by 20% PEG overnight.

          Figure 8 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left

section) upon applying a cold stress by gradually decreasing the temperature until -7°C.

Figure 9 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left section) upon applying a heat stress of 2 hours at 48°C.

Figure 10 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left section). It can be concluded that the P35S-At-DBF2 transformed plants do not show morphological abnormalities compared to the control transgenic plants.

Figure 11 shows the results of a salt stress tolerance test with transgenic *A. thaliana* plants overexpressing HSP 17.6A (A) or c74 (B). The control plants (bottom left in A and B) is a transgenic line transformed with pBIN-35S-CaMVter. The other sections in A are 5 independently obtained transgenic lines overexpressing HSP17.6A. The other sections in B are 5 independently obtained transgenic lines overexpressing c74.

Figure 12 shows the influence of *At-DBF2* expression in sense and antisense orientations on stress tolerance. BY2 cells were transformed by *A. tumefaciens* with recombinant T-DNA vectors containing *At-DBF2* driven by CaMV 35S RNA promoter, pBIN-35S-*At-DBF2* (upper left and right sections in A or diamonds in B), the CaMV 35S promoter and terminator pBIN-35S-CaMVter (bottom left sections in A or triangles in B), or antisense *At-DBF2* under the control of the CaMV 35S promoter pBIN-35S-AS*At-DBF2* (bottom right sections in A or circles in B). (A) Picture of the same amounts of transgenic cells after 3 weeks of growth on solid medium supplemented with 300 mM NaCl, 25% PEG, 2mM H<sub>2</sub>O<sub>2</sub>, or at 47°C (heat). (B) Growth of suspension cells in liquid medium. Upon stress, growth was measured as fresh weight and expressed as a percentage of unstressed growth (control) (a). Stresses were applied after subculturing (= day 0) at indicated temperatures (e) and concentrations of NaCl (b) PEG (c), and H<sub>2</sub>O<sub>2</sub> (f). For the cold shock (d), cells were maintained at 0°C for 2 days before the 2-week culture at 22°C. For each construction data of three

independent transgenic lines were pooled. To not overload the figure, SDs are not shown (maximum 15% of measured values). (C) Northern analysis of At-DBF2+TDBF2, kin1, and HSP17.6. Total RNAs were extracted from independent lines transformed with pBIN-35S-At-DBF2 (1) and (2), pBIN-35S-CaMter (3), and pBIN-35S-ASAAt-DBF2 (4). Osmotic stress was induced with 10% PEG treatment for 5 hr (stressed).

Figure 13 shows the results of the growth of *A. thaliana* plants transformed with p35S-AtHSP17.6A and P35S control (upper right section) upon applying an osmotic stress induced by 20% PEG overnight. The results of two independent experiments are shown, each performed with 3 independently obtained transgenic lines overexpressing At-HSP17.6A (upper left and bottom left and right).

Figure 14 shows the results of the germination of *A. thaliana* plants transformed with p35S-Atc74 and P35S control (bottom section) on mineral medium supplemented with 125 mM NaCl. The results of two independent experiments are shown, each performed with 2 independently obtained transgenic lines overexpressing Atc74 (2 upper sections).

20

Table 1. Classification of the *Arabidopsis thaliana* clones isolated in Example 2. Clones isolated according to the description in example 2 have been analyzed on their potential to confer tolerance. According to the method described in example 2, the tolerance of different yeast transformants expressing an Arabidopsis cDNA to osmotic stress and salt stress was compared with the tolerance of DY wild type cells.

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- + : similar growth to the DY wild type cells;
- ++ : growth of the transformant is visible at a 10-fold higher dilution (1:10) than control (1:1);
- +++ : growth of the transformant is visible at a 100-fold higher dilution (1:100) than control (1:1);
- ++++ : growth of the transformant is visible at a 1000-fold higher dilution (1:1000) than control (1:1).

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Table 2. Exemplary plant-expressible promoters for use in the performance of the present invention.

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Table 3. Exemplary stress-inducible promoters for use in the performance of the present invention.

## **EXAMPLES**

### **Example 1. Construction of the cDNA library.**

Total RNA has been isolated from green siliques from *Arabidopsis thaliana* by grinding 1 g of siliques in 4 ml extraction buffer (100 mM tris-HCl, pH 8, 10 mM EDTA, 100 mM LiCl) at 4° C, followed by phenolisation and chloroform: isoamylalcohol (24:1) extraction. To the aqueous phase, LiCl was added up to a final concentration of 2M, and the total RNA was allowed to precipitate overnight at 4°C. After centrifugation, the pellet was redissolved in 400 µl H<sub>2</sub>O and reprecipitated with ethanol. Poly(A) messenger RNA was isolated from the total RNA by binding it to an oligo-dT cellulose spun column (Pharmacia), washing the column three times with 10 mM Tris-HCl, pH 7.5, 1 mM EDTA, 0.5 M NaCl and eluting the mRNA with 10 mM Tris-HCl, pH 7.5, 1 mM EDTA at 65° C.

The eluate was precipitated with ethanol, and cDNA was synthesized using MMLV- reverse transcriptase (Pharmacia) and a d(T)<sub>14</sub>-XhoI primer for the first strand and *E. coli* DNA polymerase I (Pharmacia) for the second strand.

### **Example 2. Yeast transformation and selection for osmotolerance.**

The cDNA was cloned into pYX vectors (Ingenius, R&D systems; 2 µ based pYX 212 for bank 1, ARS/CEN based pYX112 for bank 2) as EcoRI - XhoI fragments, using an Eco RI/Not I adaptor.

In these constructs, the cDNA is under the control of the strong constitutive TPI promoter. The yeast strain DY (MATa, *his3*, *can1-100*, *ade2*, *leu2*, *trp1*, *ura3::3xSV40AP1-lacZ*; kindly provided by N. Jones, Imperial Cancer Research Fund, London, UK) has been transformed with these cDNA libraries, using the Lithium Acetate transformation procedure (Gietz and Schietsl, 1995). After transformation with the Arabidopsis cDNA bank, transformants have been selected for the ability to grow in the presence of 100mM LiCl in a stepwise selection (Lee et al., 1999). LiCl is commonly used for salt tolerance screening in yeast (Haro et al. 1991). Several *A. thaliana* genes, conferring osmotolerance to the yeast, have been isolated (Table 1). To further analyse the potential of the selected Arabidopsis cDNA's to confer tolerance to environmental stress in yeast, each yeast transformant expressing such selected Arabidopsis cDNA's has been exposed to osmotic stress and salt stress. Each of the transformants was therefore grown for 16 hours in YPD (rich medium), and cell density was adjusted to OD<sub>600</sub> at 2. Serial dilutions, 1:10, were made at three consecutive



steps. Ten microliters of each dilution was spotted on solid YPD medium (control) supplemented with 2 M sorbitol (osmotic stress) or 1.2 M NaCl (salt stress) and incubated at 28°C for 3 days. The results of this drop growth test (see also Lee et al., 1999) are shown in Table 1.

5

### Example 3. Characterization of *At-DBF2*.

*At-DBF2*, a 1.8 kb cDNA (SEQ ID NO 1) has been identified in this screening that encodes a predicted 60.2 kDa protein showing 81 % similarity with the yeast Dbf2 transcriptional regulator. Homology (less than 40% similarity) has also been found with the putative Dbf2 homologues in human, *C. elegans* and *Drosophila* (named Ndr for nuclear Dbf2 related, Millward et al. 1995). The *At-DBF2* deduced protein sequence (SEQ ID NO 2) contains the 11 domains of protein kinases (Figure 1A). Amino acids lying between the invariant residues D and N of domain VI do not match the features of serine/threonine specificity (LKPE) defined by Hanks et al. (1988) but the GSPDYIALE peptide in domain VIII does well indicate serine/threonine specificity and *At-DBF2* can complement the yeast *dbf2* mutant (Figure 1B).

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In mature *Arabidopsis* plants, *At-DBF2* is expressed in all tested organs. The highest abundance of transcripts has been found in siliques. A Southern analysis in *Arabidopsis*, tobacco and tomato has revealed that *DBF2* seems to be conserved in plants (see Example 13 below). As *At-DBF2* has been identified in a screening for LiCl tolerance, its effect in other stress situations has been tested in yeast (Figure 2).

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### Example 4. Overexpression of *Arabidopsis* and *Saccharomyces cerevisiae DBF2* enhances cold, heat, salt and drought tolerance in yeast.

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In order to test whether the effect was specific to the plant gene, the yeast *DBF2* gene has been overexpressed in the same vector. Upon a drop growth test (Figure 2 and Lee et al., 1999). A remarkable enhancement of stress tolerance can be seen at 42°C, during osmotic stress (sorbitol), and after salt and cold treatments in yeast. There is no difference between stress tolerance afforded by the plant or the yeast gene. The enhancement of stress tolerance due to the overexpression of *At-DBF2* or *DBF2* reflects a role for these genes in stress situations. Therefore yeast and *Arabidopsis* plants have been exposed to sorbitol- and PEG-induced osmotic stress. *At-DBF2* as well as *DBF2* is induced rapidly (1 to 2 hours) and transiently upon osmotic stress (Figure 3A). The expression of *At-DBF2* and *DBF2* has been analyzed during other environmental stresses in *Arabidopsis* plants or in yeast cells after the

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time corresponding to the highest induction seen in Fig. 3A (Figure 3B). In plant as in yeast, there is a clear induction after heat, salt, osmotic and to a lesser extent after cold, which perfectly correlates with stresses to which the overexpression enhances tolerance. However, many genes are induced upon stress without relevant adaptive role, amongst others because post-transcriptional mechanisms inhibit subsequent translation. Here *At-DBF2* protein amount, as detected by anti-Dbf2 antibodies, clearly increased upon stress (Figure 3C).

**Example 5. Both *At-DBF2* and *DBF2* can functionally complement the *hog1* mutation.**

To investigate a possible interaction between stress signaling pathways and *DBF2*, the salt sensitive *hog1* mutant was transformed with *At-DBF2* and *DBF2*. The *HOG1* MAP kinase pathway regulates osmotic induction of transcription in yeast (Schuller *et al.* 1994). The osmosensitivity of the mutant could be recovered by the overexpression of both *DBF2* and *At-DBF2* (Figure 4).

**Example 6. *At-DBF2* is cell cycle regulated.**

*DBF2* expression is cell cycle regulated where it plays a role in DNA synthesis initiation but also in nuclear division through its association with the CCR4 complex (Komarnitsky *et al.* 1998, Johnston *et al.* 1990). This regulation was investigated in plants. A tobacco BY-2 cell line in which the highest level of culture synchronization, compared with other plant cell lines has been achieved so far (Shaul *et al.* 1996, Reicheld *et al.* 1995) was used. Stationary phase cells were diluted into fresh medium and treated with aphidicolin (blocking cells in the beginning of the S phase) for 24 hours, then washed. The percentage of synchronous mitosis after release from the aphidicolin block was about 65 % (Figure 5A-B). A 1.6-Kb tobacco *DBF2* homologue (*T-DBF2*) could be detected on Northern blot with the *At-DBF2* as a probe. *T-DBF2* steady-state transcript level clearly oscillates during the cell cycle and is mainly present during S, decreases during G2 until late M from where it increases until a peak in S phase. *T-DBF2* expression occurs clearly before *CYCB1.2* (a marker of G2-M phases), but parallels the one of H4 (a S phase marker) except at the S/G2 transition, where *T-DBF2* transcripts decline earlier, and at the M/G1 transition, where *T-DBF2* expression increases earlier. The use of the cell cycle markers *CYCB1.2* and H4 is described in Reicheld *et al.*

To follow unperturbed G1 and S phases, BY2 cell suspension was synchronized using a double blocking procedure (Nagata *et al.*, 1992). After the release from the aphidicoline block, cells are treated for 4 hours with propyzamide in the beginning of the preprophase. The percentage of synchronous mitosis after the release from the propyzamide block was higher than 75%. *T-DBF2* was periodically expressed with an undetectable expression until late M, a sharp increase in G1 and a peak in mid S (Figure 5C-D) which confirms results of Figures 5A-B. However a function for the plant *DBF2* in cell cycle can only be assigned with measurement of the kinase activity. In yeast, *DBF2* transcript levels do not correlate with kinase activation which occurs by dephosphorylation (Toyn and Johnson, 1994). The precise function of Dbf2 in regulation of the cell cycle is not known. An essential role has been proposed during anaphase or telophase. No activity has been measured in G1 despite evidence for a role for Dbf2 in initiation of DNA synthesis.

As other proteins recently identified, Dbf2 controls the M/G1 transition which is a major cell cycle transition in yeast (Aerne *et al.* 1998). The existence of a M/G1 control checkpoint has been suggested in plant cells (Hemmerlin and Bach 1998) but its importance compared to G1/S and G2/M has not been investigated.

Overexpression of *DBF2* in yeast results in kinase activity throughout the cell cycle, which may be due to the saturation of a post-translational deactivating mechanism (Toyn and Johnston, 1994). Overexpression of the functionally conserved *At-DBF2* has most probably the same effect. However, the presence of Dbf2 kinase activity at the wrong time in the cell cycle does apparently not affect its progression. In marked contrast constitutive activity has a marked effect on stress tolerance. The role played by *At-DBF2* or *DBF2* in stress is most probably independent from the cell division cycle. *At-DBF2* expression is present in all plant organs (abundant expression is observed in stems where only 1-2 % cells have a mitotic activity) and can be rapidly induced upon stress. However, a link with the cell cycle is not excluded. Higher stress tolerance in yeast overexpressing *DBF2* or *At-DBF2* may be correlated to the overproduction of the kinase in G1 where yeast cells are particularly sensitive to stress. Most plant cells are also thought to be blocked in G1 but the relationship with stress response is poorly known.

**Example 7. Tobacco cell transformation and recombinant T-DNA Vector construction**

BY2 cells were stably transformed as described (Shaul et al., 1996) by *Agrobacterium tumefaciens* C58C1Rif<sup>R</sup> (pGV2260) strain (Deblaere et al., 1985) carrying pBIN-35S-At-DBF2 or pBIN-35S-ASAt-DBF2 recombinant binary vectors. PBIN-35S-At-DBF2 is the plant binary vector pBIN m-gfp4 in which the BamHI-SacI fragment containing the gfp reporter gene was replaced with a BamHI-SacI fragment containing the At-DBF2 cDNA from pYX-At-DBF2. p-Bin-35S-CaMVter is the plant binary vector pBIN19 in the HindIII-SacI restriction sites of which the hindIII-SacI fragment of pDH51 containing the cauliflower mosaic virus (CaMV) 35S RNA promoter and terminator was cloned. pBIN-35S-ASAt-DBF2 is the pBIN-35S-CaMVter vector in which the At-DBF2 cDNA was cloned in the antisense orientation from pYXAt-DBF2 in the BamHI-SmaI restriction sites, between the CaMV 35S RNA promoter and terminator. More details are described in Lee et al. (1999).

**Example 8. Overexpression of At-DBF2 sense and antisense RNA in plant cells**

Transgenic plant cells overexpressing *At-DBF2* were generated to test the role of this protein in stress tolerance *in planta*. Tobacco BY2 cells were stably transformed by *A. tumefaciens* carrying the *At-DBF2* cDNA driven by the strong constitutive CaMV 35S RNA promoter. The antisense *At-DBF2* RNA also was overexpressed under the control of the same promoter. Control lines were obtained by transforming tobacco BY2 cells with pBIN-35S-CaMVter. Three independently obtained *At-DBF2*-overexpressing tobacco transgenic cell lines have been selected with a high and similar *At-DBF2* expression and analysed further. Three tobacco transgenic cell lines overexpressing antisense *At-DBF2* were chosen that showed an undetectable tobacco DBF2 transcript level. Both the overexpression of *At-DBF2* and the down-regulation of the endogenous gene by the antisense strategy did not result in significant differences in growth after 2 weeks (Fig. 12A and 12B). On the contrary, marked differences in growth were observed after a 2-week treatment with NaCl, PEG-induced drought, cold, or high temperatures. Transgenic lines that overexpressed *At-DBF2* were clearly more tolerant than control lines. Inhibition of the endogenous DBF2 expression was correlated with a higher sensitivity to those stresses. To understand the basis of stress

tolerance in *At-DBF2*-overexpressing plant cells, expression of stress-induced genes was followed in control and stress conditions (Fig. 12C). Tobacco kin1 and HSP17.6A homologues already were induced in *At-DBF2*-overexpressing tobacco cells in control conditions to a level similar to that observed during stress conditions (PEG-induced drought), suggesting that *At-DBF2* overexpression may mimic a stress signal.

#### **Example 9. Arabidopsis transformation and recombinant T-DNA vector construction with genes conferring tolerance to environmental stress**

Arabidopsis were stably transformed as described in Clarke, Wei and Lindsey (1992) by *Agrobacterium tumefaciens* C58C1RifR (pGV2260) strains carrying pBIN-35S-*At-DBF2*, pBIN-35S-*At-HSP17.6A*, pBIN-35S-*At-c74* recombinant binary vectors. pBIN-35S-*At-DBF2* is described in Lee et al. 1999. pBIN-35S-*At-HSP17.6A* recombinant binary vector was constructed as following: the EcoRI-XhoI fragment containing *At-HSP17.6A* cDNA in pYX-HSP17.6A (recombinant pYX212) was first cloned in pYES2 (Invitrogen) resulting in pYES-HSP17.6A. Then the BamHI-SphI fragment of pYES-HSP17.6A containing the *At-HSP17.6A* cDNA was cloned in the plant binary vector pBIN m-gfp4 in which the BamHI-SacI fragment containing the *gfp* receptor gene was deleted and replaced by the *At-HSP17.6A* cDNA. The 3' protruding ends generated by SacI and SphI were blunt ended by T4 DNA polymerase. pBIN-35S-*c74* was constructed with a similar strategy as pBIN-35S-*AtHSP17.6A* with an intermediary pYES-*Atc74* vector. The *At-c74* cDNA was first amplified with PCR using the primers 5' AAA AAA CAC ATA CAG GAA TTC 3' (SEQ ID NO 122) and 5' AGT TAG CTA GCT GAG CTC GAG 3' (SEQ ID NO 123), then cloned "blunt ended" in the vector pYES2 cut with NotI and BstXI and blunt ended with T4 DNA polymerase. Subsequently, the BamHI-SphI fragment of pYES-*c74* was cloned in pBINm-gfp4 as explained supra.

#### **Example 10. Tolerance to environmental stress in plant cells**

Transgenic calli were isolated from each of the transgenic Arabidopsis lines transformed with *At-DBF2*, *At-HSP17.6A* and *At-c74*. The growth of these transgenic calli during salt stress was measured and compared with control calli derived from transgenic Arabidopsis lines transformed with pBIN-35S-*CaMVter*. Callus pieces (25 for each transgenic line) of similar fresh weight (50 to 100 mg) were therefor grown on callus inducing medium (Clarke et al., 1992) supplemented with 200mM NaCl. After two weeks, from visual inspection, it was clear that transgenic calli transformed with



At-DBF2 or At-HSP17.6A or At-c74 looked much better than control transgenic calli transformed with pBIN-35S-CaMVter. The latter calli turned yellow and started dying. To confirm the observation, the fresh weight of the calli was measured. In comparison with the control transgenic calli, the fresh weight of the transgenic calli was for each of the three lines at least five times higher than the fresh weight of the control transgenic calli.

#### **Example 11. Tolerance to environmental stress in plants.**

Seeds from transgenic Arabidopsis plants transformed with pBIN-35S-At-DBF2, p-BIN-35S-At-c74, or pBIN-35S-At-HSP17.6A, were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-AS+At-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark, 70 microeinsteins. After 9 days growth, filters were transferred to liquid K1 medium supplemented with 200 mM NaCl for overnight incubation. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium. Under these conditions, the control transgenic plants turned yellow, their growth was inhibited and eventually they died. On the contrary, the transgenic lines transformed with At-DBF2 or At-HSP17.6A or At-c74 survived very well (Figure 6 and Figure 11).

To further evaluate the scope of protection to environmental stress, transgenic plants were exposed to osmotic stress. Therefor seeds from transgenic Arabidopsis plants transformed with pBIN-35S-At-DBF2, pBIN-35S-At-c74 or pBIN-35S-At-HSP17.6A were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-ASAt-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark,

70 microeinsteins. After 9 days growth, filters were transferred to liquid K1 medium supplemented with 20 % polyethylene glycol for overnight incubation. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium. Under these conditions, the control transgenic plants turned yellow, their growth was inhibited and eventually they died. On the contrary, the transgenic lines transformed with At-DBF2, At-HSP17.6A or At-c74 survived very well (see Figure 7 and 13). Their growth was comparable to growth on control medium without polyethylene glycol.

To further analyse the scope of protection to environmental stress, transgenic plants were exposed to high and low temperatures. Therefor seeds from transgenic plants transformed with pBIN-35S-At-DBF2 or pBIN-35S-At-c74 were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-ASAAt-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark, 70 microeinsteins. After 9 days growth, for the experiments with high temperature stress, plants were exposed to 48°C for two hours. For the experiments with low temperature stress, plants were exposed to gradually decreasing temperatures, down to -7°C. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium.

Under both low temperature and high temperature stress, the growth of control transgenic plants was inhibited and eventually they died. The transgenic lines transformed with At-DBF2 or At-c74 survived very well. Their growth was comparable to growth under control conditions with normal temperature (see Figure 8 and 9).

To further analyse the scope of protection to environmental stress, transgenic plants were exposed to salt stress during germination. Sterilized mature seeds from transgenic plants transformed with pBIN-35S-At-DBF2 or pBIN-35S-At-c74 were placed on top of petri dishes containing MS (Murashige and Skoog) medium with 0,8 % agar and 30 g l<sup>-1</sup> sucrose. Control plants were the ones transformed with pBIN-35S-CaMVter. Prior to germination and pH 5.7 adjustment, NaCl was added to a final concentration of 125 mM. Three petri dishes with a mean of 40-50 seeds per dish were used per treatment in every experiment. The complete experiment was repeated

twice. Seed germination at 22°C was followed. Seeds were considered to germinate after radical and green cotyledon emergency occurred.

On control medium (without 125 mM NaCl), germination of all transgenic lines was very similar to each other and to wild type plants. On medium supplemented with 125 mM NaCl, seeds from transgenic lines overexpressing At-DBF2 or At-c74 germinate significantly better than control transgenic lines. Less than 10 % of the seeds from transgenic lines transformed with pBIN-35S-CaMVter germinate under these conditions. In contrast, more than 70 % of the seeds from transgenic lines overexpressing At-DBF2 or At-c74 germinate on medium containing 125 mM NaCl (Figure 14).

#### Example 12. Southern hybridisation of At-DBF2 genes in other plants

To investigate whether *DBF2* homologues exist in other plant species, a Southern hybridisation analysis was performed using the full length *At-DBF2* as a probe. Genomic DNA was extracted from tobacco, tomato and rice according to Dellaporta et al. (1983) and further purified by phenol :chloroform extractions.

DNA (10 µg) was digested with restriction enzymes and separated on 1% (w/v) agarose gels using Lambda DNA digested with Hind III as molecular size standards. The DNA was transferred on to nylon membranes (Hybond N ; Amersham, little Chalfont, UK) in 0.4 N NaOH. Filters were UV-cross-linked for 30 seconds, prehybridized for 3 hours at 56°C in hybridization solution (2x SSPE, 0.1%(w/v) SDS, 5x Denhardt solution) using 200 gm<sup>-3</sup> denatured salmon sperm DNA, and hybridized overnight with radiolabelled probes. 1X SSPE was 0.15 M NaCl/ 0.01 M sodium dihydrogen phosphate/ 1 mM EDTA.

Filters were washed at 56°C in 2x SSPE, 0.1% (w/v) SDS for 20 min, then 1x SSPE, 0.1% (w/v) SDS for 20 min, and finally in 0.1x SSPE, 0.1% (w/v) SDS for 20 min. Filters were exposed to X-ray film (Kodak X-AR ; Kodak, NY, USA) in the presence of intensifying screens for 24 hours.

The results of the hybridisation experiments show that tobacco, tomato and rice have at least one homologue to At-DBF2.

**Tabel 1**

putative function in	Features of encoded protein	SEQ ID NO.	Growth on medium with 1,2 M NaCl	growth on medium with 2,0 M sorbitol
signalling	Similar to a yeast DBF2 cell cycle protein	1	++++	++++
metabolism	HSP17.6A	3	++++	++++
unknown	C74	5	+++	+++
metabolism	Similar to ADH2	7	+	++++
metabolism	Similar to D. melanogaster catalase/catalase 3	9	++++	+
metabolism	Similar to the HSP90 heat shock protein family	11	++++	++++
metabolism	similar to phosphoenolpyruvate carboxylase	13	+	+++
metabolism	pathogen related proteins, class 10	15	+	++++
metabolism	Arabidopsis ascorbate peroxidase	17	++++	++++
metabolism	similar to phosphatase binding protein	19	++++	++++
metabolism	similar to phosphatase binding protein	21	++++	++++
metabolism	similar to retinol dehydrogenase	23	+++	++++
metabolism	similar to retinol dehydrogenase	25	++++	++++
metabolism	ribosomal protein	27	++++	++++
metabolism	ribosomal protein	29	++++	++++
metabolism	similar to a protein transporter (kinase homolog)	31	++++	++++
metabolism	similar to a peptide transporter	33	++++	+
metabolism	similar to a wheat low affinity cation transporter LCT1	35	++++	++++
metabolism	similar to yeast iso-1-cytochrome c (CYC-1)	37	++++	++++
metabolism	similar to yeast OSM1	39	++++	++++
metabolism	similar to yeast copper uptake gene (CUP1)	41	++++	+++
metabolism	similar to yeast UV-induced damage repair protein (RAD7)	43	++++	++++
metabolism	electron transporter, apocytochrome b	45	++++	++++
metabolism	similar to membrane lipoprotein LPPL1	47	++++	++++
metabolism	similar to tobacco auxin binding protein	49	+	++++
metabolism	similar to tobacco cytokinin binding protein CBP 57	51	+++	++++
signalling	similar to calcium binding protein yeast calcineurin B	53	+++	++++

signalling	similar to calcium binding protein glycine max calnexin	55	++++	+++
signalling	similar to calcium binding protein Dictyostelium discoideum calreticulin	57	++++	++++
signalling	similar to calcium binding protein calmodulin 1	59	++++	+
signalling	similar to calcium binding protein calmodulin 2	61	+	++++
signalling	MAP kinase kinase, homologous to Dyctyostelium mekA (DdMek1)	63	++++	+++
signalling	similar to human adenosine kinase	65	+	++++
signalling	similar to human tyrosine kinase	67	++++	++++
signalling	similar to common ice plant tyrosine kinase	69	++++	++++
signalling	similar to the yeast protein kinase C receptor	71	++++	++++
signalling	similar to tobacco and Arabidopsis HAT7 homeotic protein	73	++	++++
signalling	similar to E. coli sigma factor regulator (RSEB)	75	+	++++
signalling	similar to human protein phosphatase 2C	77	++++	++++
metabolism	late embryogenesis abundant proteins, Arabidopsis LEA protein 10 & 14	79	++	++++
metabolism	late embryogenesis abundant proteins, Arabidopsis LEA protein 10 & 14	81	++	++++
metabolism	pathogen related proteins, class 10	83	++++	++++
metabolism	cell wall peroxidase	85	++++	+++
metabolism	ribosomal protein	87	+++	++++
metabolism	salt stress induced protein, SAS 1	89	++++	++++
metabolism	PR gene (AIG2)	91	++++	++++
metabolism	MT1c	93	++++	++++
metabolism	IPP2 (Isopentenyl diphosphate)	95	+++	++++
metabolism	chlorophyll a/b binding protein	97	+++	+++
metabolism	glutathione transferase	99	++	++++
signalling	cold- and ABA inducible, calcium dependent – kinase, Kin1	101	++++	++++
signalling	MAP kinase, Atmpk1	103	++	++++
signalling	Arabidopsis cell cycle protein histone H2A	105	++++	++++
unknown	chromosome 4 – sequence	107	+++	++++
unknown	chromosome 4 – sequence	109	+	++++
unknown	chromosome 5 – sequence	111	++++	+++
unknown	chromosome 5 – sequence	113	++++	++
unknown	chromosome 5 – sequence	115	++++	++++
unknown	chromosome 5 – sequence	117	+	++++
unknown	chromosome 5 – sequence	119	+	++++



signalling	similar to calcium binding protein centrin (caltractin)	121	++++	++++
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**TABLE 2**  
**EXEMPLARY PLANT-EXPRESSIBLE PROMOTERS FOR USE IN THE PERFORMANCE OF**  
**THE PRESENT INVENTION**

GENE SOURCE	EXPRESSION PATTERN	REFERENCE
$\alpha$ -amylase ( <i>Amy32b</i> )	Aleurone	Lanahan <i>et al</i> (1992); Skriver <i>et al.</i> (1991)
cathepsin $\beta$ -like gene	Aleurone	Cejudo <i>et al.</i> (1992)
<i>Agrobacterium rhizogenes</i> <i>rolB</i>	Cambium	Nilsson <i>et al.</i> (1997)
PRP genes	cell wall	<a href="http://salus.medium.edu/mmg/tierney/html">http://salus.medium.edu/mmg/tierney/html</a>
barley <i>lir1</i> promoter	Endosperm	
synthetic promoter	Endosperm	Vicente-Carbajosa <i>et al.</i> (1998)
AtPRP4	Flowers	<a href="http://salus.medium.edu/mmg/tierney/html">http://salus.medium.edu/mmg/tierney/html</a>
chalcone synthase ( <i>chsA</i> )	Flowers	van der Meer <i>et al.</i> (1990)
<i>apetala-3</i>	Flowers	
Chitinase	fruit (berries, grapes, etc)	Thomas <i>et al.</i> CSIRO Plant Industry, Urrbrae, South Australia, Australia; <a href="http://winetitles.com.au/gwrdc/csh95-1.html">http://winetitles.com.au/gwrdc/csh95-1.html</a>
<i>rbcS-3A</i>	green tissue (eg leaf)	Lam <i>et al.</i> (1990); Tucker <i>et al.</i> (1992)
leaf-specific genes	Leaf	Baszczynski <i>et al.</i> (1988)
AtPRP4	Leaf	<a href="http://salus.medium.edu/mmg/tierney/html">http://salus.medium.edu/mmg/tierney/html</a>
<i>Pinus cab-6</i>	Leaf	Yamamoto <i>et al.</i> (1994)
SAM22	Senescent leaf	Crowell <i>et al.</i> (1992)
<i>R. japonicum nif</i> gene	Nodule	United States Patent No. 4, 803, 165
<i>B. japonicum nifH</i> gene	Nodule	United States Patent No. 5, 008, 194

GmENOD40	Nodule	Yang <i>et al.</i> (1993)
PEP carboxylase (PEPC)	Nodule	Pathirana <i>et al.</i> (1992)
Leghaemoglobin (Lb)	Nodule	Gordon <i>et al.</i> (1993)
<i>Tungro bacilliform</i> virus gene	Phloem	Bhattacharyya-Pakrasi <i>et al.</i> (1992)
sucrose-binding protein gene	plasma membrane	Grimes <i>et al.</i> (1992)
pollen-specific genes	pollen; microspore	Albani <i>et al.</i> (1990); Albani <i>et al.</i> (1991)
maize pollen-specific gene	Pollen	Hamilton <i>et al.</i> (1992)
sunflower pollen-expressed gene	Pollen	Baltz <i>et al.</i> (1992)
<i>B. napus</i> pollen-specific gene	pollen; anther; tapetum	Arnoldo <i>et al.</i> (1992)
root-expressible genes	Roots	Tingey <i>et al.</i> (1987); An <i>et al.</i> (1988);
tobacco auxin-inducible gene	root tip	Van der Zaal <i>et al.</i> (1991)
$\beta$ -tubulin	Root	Oppenheimer <i>et al.</i> (1988)
Tobacco root-specific genes	Root	Conkling <i>et al.</i> (1990)
<i>B. napus</i> G1-3b gene	Root	United States Patent No. 5, 401, 836
SbPRP1	Roots	Suzuki <i>et al.</i> (1993)
AtPRP1; AtPRP3	roots; root hairs	<a href="http://salus.medium.edu/mmg/tierney/html">http://salus.medium.edu/mmg/tierney/html</a>
RD2 gene	root cortex	<a href="http://www2.cnsu.edu/ncsu/research">http://www2.cnsu.edu/ncsu/research</a>
TobRB7 gene	root vasculature	<a href="http://www2.cnsu.edu/ncsu/research">http://www2.cnsu.edu/ncsu/research</a>
AtPRP4	leaves; flowers; lateral root primordia	<a href="http://salus.medium.edu/mmg/tierney/html">http://salus.medium.edu/mmg/tierney/html</a>
Seed-specific genes	Seed	Simon <i>et al.</i> (1985); Scofield <i>et al.</i> (1987); Baszczyński <i>et al.</i> (1990)
Brazil Nut albumin	seed	Pearson <i>et al.</i> (1992)
Legumin	Seed	Ellis <i>et al.</i> (1988)
Glutelin (rice)	Seed	Takaiwa <i>et al.</i> (1986); Takaiwa <i>et al.</i>

		(1987)
Zein	Seed	Matzke <i>et al.</i> (1990)
NapA	Seed	Stalberg <i>et al.</i> (1996)
Sunflower oleosin	seed(embryo and dry seed)	Cummins <i>et al.</i> (1992)
<i>LEAFY</i>	shoot meristem	Weigel <i>et al.</i> (1992)
<i>Arabidopsis thaliana knat1</i>	shoot meristem	Accession number AJ131822
<i>Malus domestica kn1</i>	shoot meristem	Accession number Z71981
<i>CLAVATA1</i>	shoot meristem	Accession number AF049870
Stigma-specific genes	Stigma	Nasrallah <i>et al.</i> (1988); Trick <i>et al.</i> (1990)
Class I patatin gene	Tuber	Liu <i>et al.</i> (1991)
<i>Blz2</i>	Endosperm	EP99106056.7
PCNA rice	Meristem	Kosugi <i>et al.</i> (1991); Kosugi and Ohashi (1997)

Table 3. Stress inducible promoters

Name	Stress	Reference
P5CS (delta(1)-pyrroline-5-carboxylate syntase)	salt, water	Zhang et al; Plant Science. Oct 28 1997; 129(1): 81-89
cor15a	Cold	Hajela et al., Plant Physiol. 93: 1246-1252 (1990)
cor15b	Cold	Wlihelm et al., Plant Mol Biol. 1993 Dec; 23(5):1073-7
cor15a (-305 to +78 nt)	cold, drought	Baker et al., Plant Mol Biol. 1994 Mar; 24(5): 701-13
rd29	salt, drought, cold	Kasuga et al., Nature Biotechnology, vol 18, 287-291, 1999
heat shock proteins, including artificial promoters containing the heat shock element (HSE)	Heat	Barros et al., Plant Mol Biol, 19(4): 665-75, 1992. Marrs et al., Dev Genet., 14(1): 27-41, 1993. Schoffl et al., Mol Gen Gent, 217(2-3): 246-53, 1989.
smHSP (small heat shock proteins)	heat	Waters et al, J Experimental Botany, vol 47, 296, 325-338, 1996
wcs120	Cold	Ouellet et al., FEBS Lett. 423, 324-328 (1998)
ci7	Cold	Kirch et al., Plant Mol Biol, 33(5): 897-909, 1997 Mar
Adh	cold, drought, hypoxia	Dolferus et al., Plant Physiol, 105(4): 1075-87, 1994 Aug
pws18	water: salt and drought	Joshee et al., Plant Cell Physiol, 39(1): 64-72, 1998, Jan
ci21A	Cold	Schneider et al., Plant Physiol, 113(2): 335-45, 1997
Trg-31	Drought	Chaudhary et al., Plant Mol Biol, 30(6): 1247-57, 1996
Osmotin	Osmotic	Raghothama et al., Plant Mol Biol, 23(6): 1117-28, 1993

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**Claims**

1. A method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.
2. An isolated polynucleic acid obtainable by a method according to claim 1.
3. The isolated polynucleic acid of claim 2 which encodes a polypeptide as listed in Table 1.
4. The isolated polynucleic acid of claim 3, which is chosen from:
  - (a) any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121, or the complementary strands thereof;
  - (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
  - (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
  - (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).
5. The isolated polynucleic acid of any of claim 2 to 4, which encodes a plant homolog of yeast DBF2 kinase.
6. The isolated polynucleic acid of claim 5, which is chosen from:
  - (a) SEQ ID NO 1, or the complementary strands thereof;
  - (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;



- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

5

7. Use of an isolated polynucleic acid of claims 2 to 3 which encodes an HSP 17.6A protein for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

10 8. Use of an isolated polynucleic acid of claim 7 for expression of the protein encoded thereby in a plant cell, with said polynucleic acid being chosen from:

15

- (a) SEQ ID NO 3, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

20

9. Use of an isolated polynucleic acid as defined above which is chosen from:

25

- (a) any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

30

for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

35

10. The isolated polynucleic acid of any of claims 2 to 4, which encodes a c74 protein which is chosen from:

- 5
- (a) SEQ ID NO 5, or the complementary strand thereof;
  - (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
  - (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
  - 10 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

11. An isolated polypeptide encoded by a polynucleic acid according to or as defined in any of claims 2 to 10, or a functional fragment thereof.

15

12. The isolated polypeptide of claim 11 having at least part of the sequence of any of SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120.

20

13. A method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising transiently introducing into a plant cell a recombinant DNA comprising a polynucleic acid of or as defined in any of claims 2 to 10 which is expressed in an amount effective to confer enhanced tolerance or resistance to environmental stress.

25

14. A method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising stably introducing into a plant cell a recombinant DNA comprising a polynucleic acid of or as defined in any of claims 2 to 10 which is expressed in an amount effective to confer enhanced tolerance or resistance to environmental stress.

30

15. The method of claims 13 or 14 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claims 5 or 6 encoding a plant DBF2 kinase.
- 5
16. The method of claim 16 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claims 7 or 8 encoding an HSP 17.6A protein.
- 10
17. The method of claim 13 to 14 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claim 10 encoding a c74 protein.
18. The method of any of claims 13 to 17, comprising introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:
- 15
- a polynucleic acid according to or as defined in any of claims 2 to 10, and,
  - a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter.
- 20
19. A method for producing a plant with enhanced tolerance or resistance to environmental stress, comprising introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:
- 25
- a DNA encoding a protein which when expressed in said plant cell at an effective amount indirectly increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or indirectly increases or induces the activity of a polypeptide of claims 11 or 12, and,
- 30

- a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.

- 5 20. A method of claim 19 wherein said DNA encodes a sense or antisense RNA molecule or a ribozyme capable of increasing or inducing the expression of said endogenous polynucleic acid sequence according to or as defined in any of claims 2 to 10.
- 10 21. A recombinant polynucleic acid comprising:  
a polynucleic acid according to or as defined in any of claims 2 to 10, and,  
a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter.
- 15 22. A recombinant polynucleic acid comprising:  
(a) a DNA encoding a protein which when expressed in said plant cell at an effective amount increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or increases or induces the activity of a polypeptide of claims 11 or 12, and,  
20 (b) a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.
23. The recombinant polynucleic acid of claim 22, wherein said DNA encodes an anti-sense RNA, a ribozyme or a sense RNA which when expressed in a cell of a plant  
25 increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or which induces or increases the activity of a protein of claim 11 or 12.
24. The recombinant polynucleic acid of claim 21 comprising at least part of the  
30 nucleotide sequence of any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, or part thereof.

25. The recombinant polynucleic acid of claim 21 to 24 comprising at least part of the coding sequence of a gene encoding a protein as listed in Table 1.
- 5 26. The recombinant polynucleic acid of any of claims 21 to 25 wherein said plant-expressible promoter is a constitutive promoter.
27. The recombinant polynucleic acid of any of claims 21 to 25 wherein said plant-expressible promoter is a stress-inducible or organ- or tissue-specific promoter.
- 10 28. The recombinant polynucleic acid of any of claims 21 to 26 wherein said plant-expressible promoter is the 35S promoter of CaMV.
29. A recombinant host cell transformed with at least one isolated polynucleic acid of or as defined in any of claims 2 to 10.
- 15 30. A plant cell transformed with a recombinant polynucleic acid of any one of claims 21 to 28.
31. A plant consisting essentially of plant cells of claim 30.
- 20 32. A callus consisting essentially of plant cells of claim 30.
33. A harvestable part, organ, tissue or propagation material of a plant of claim 31, comprising said recombinant DNA.
- 25 34. The use of a recombinant polynucleic acid of claim 21 to 28 to produce transgenic plants.
- 30 35. A probe which is part of the polynucleic acid sequence of or as defined in any of claims 2 to 10 and which hybridizes specifically with said polynucleic acid or the complement thereof.
- 35 36. A primer which is part of the polynucleic acid sequence of or as defined in any of claims 2 to 10 and which specifically amplifies said polynucleic acid or the complement thereof.



37. A composition comprising a polynucleic acid sequence of or as defined in any of claims 2 to 10, a polypeptide of claim 11 or 12, a probe of claim 35 or a primer of claim 36.

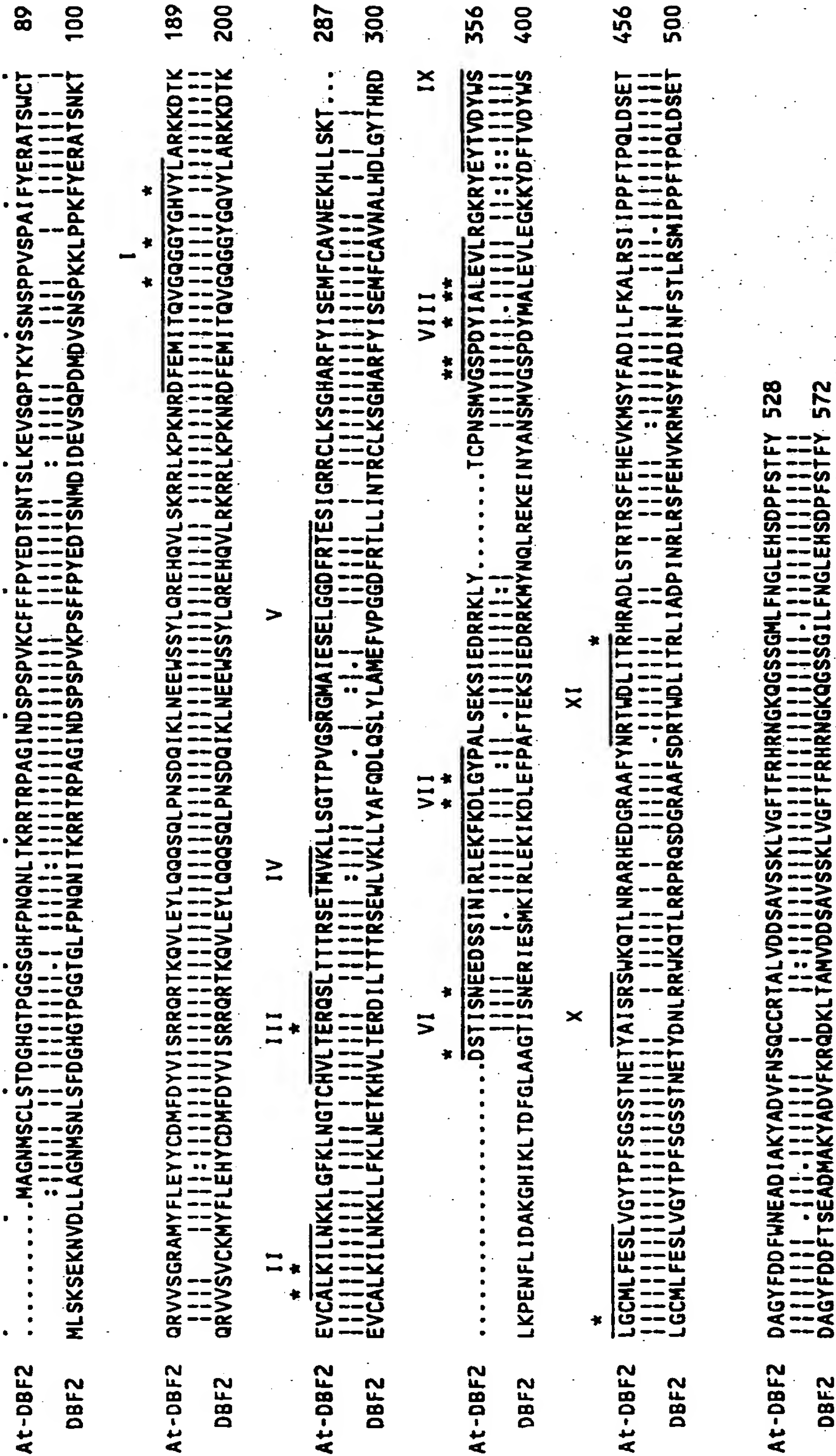


FIGURE 1 A

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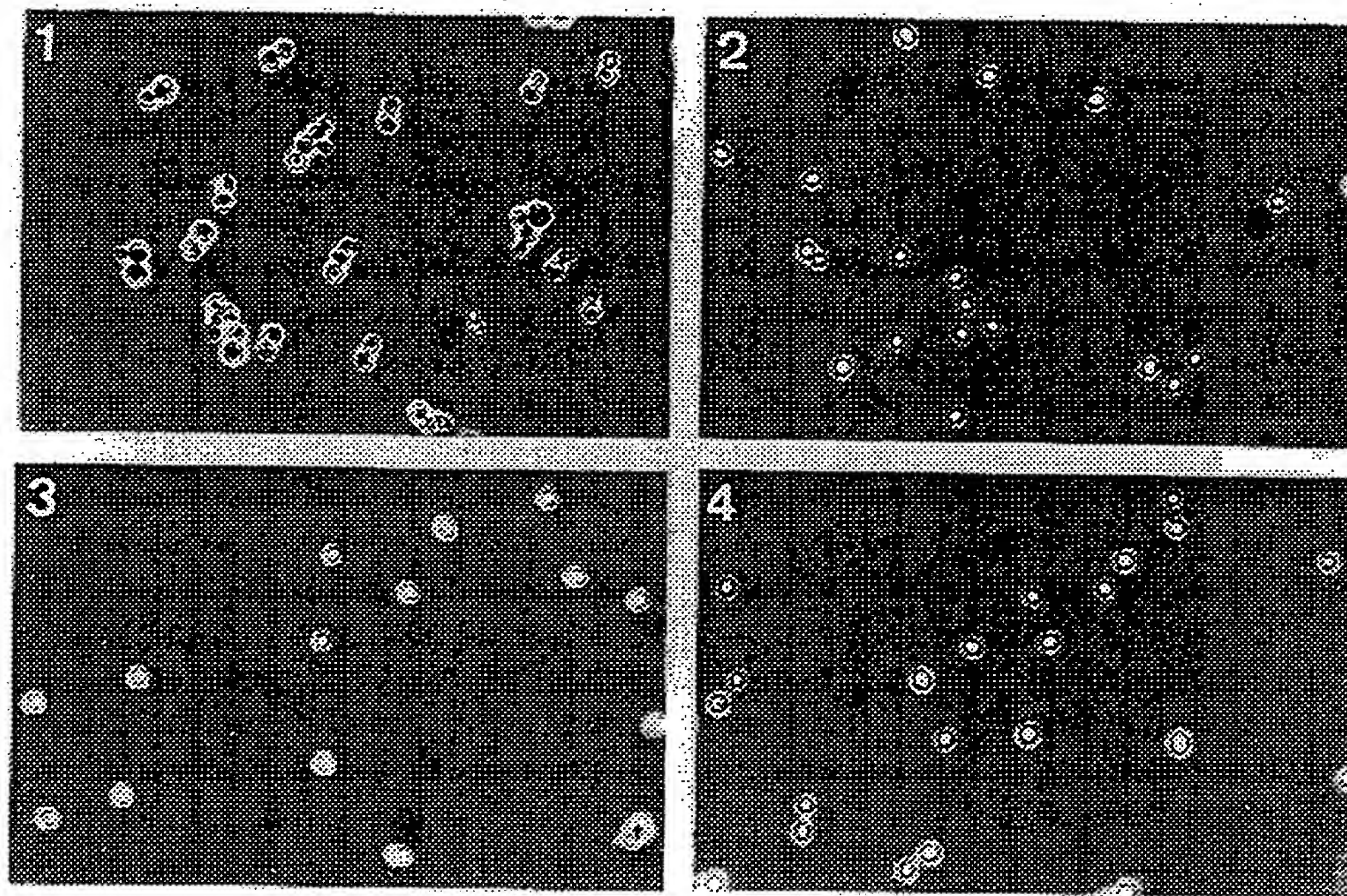


FIGURE 1B

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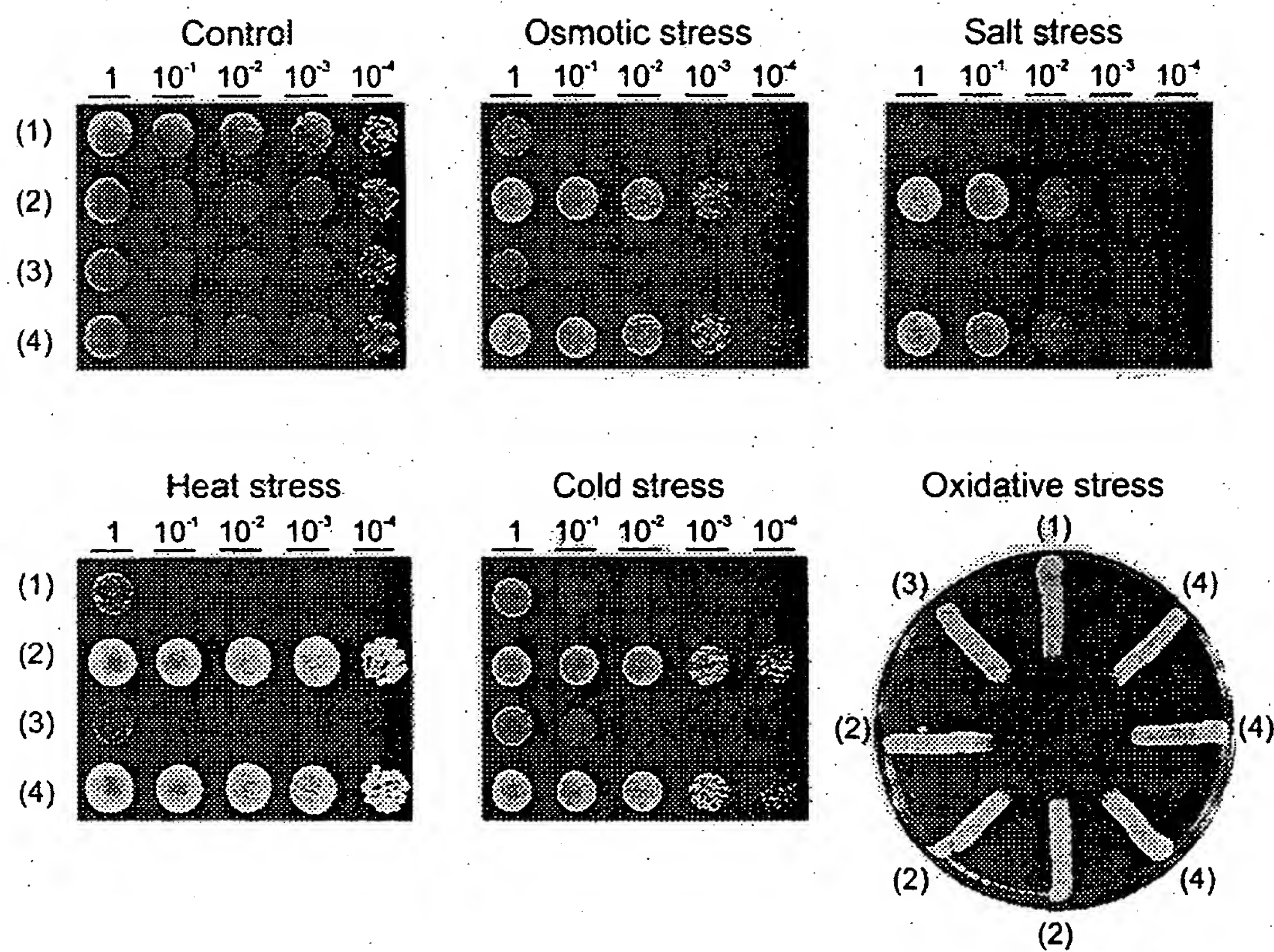


FIGURE 2



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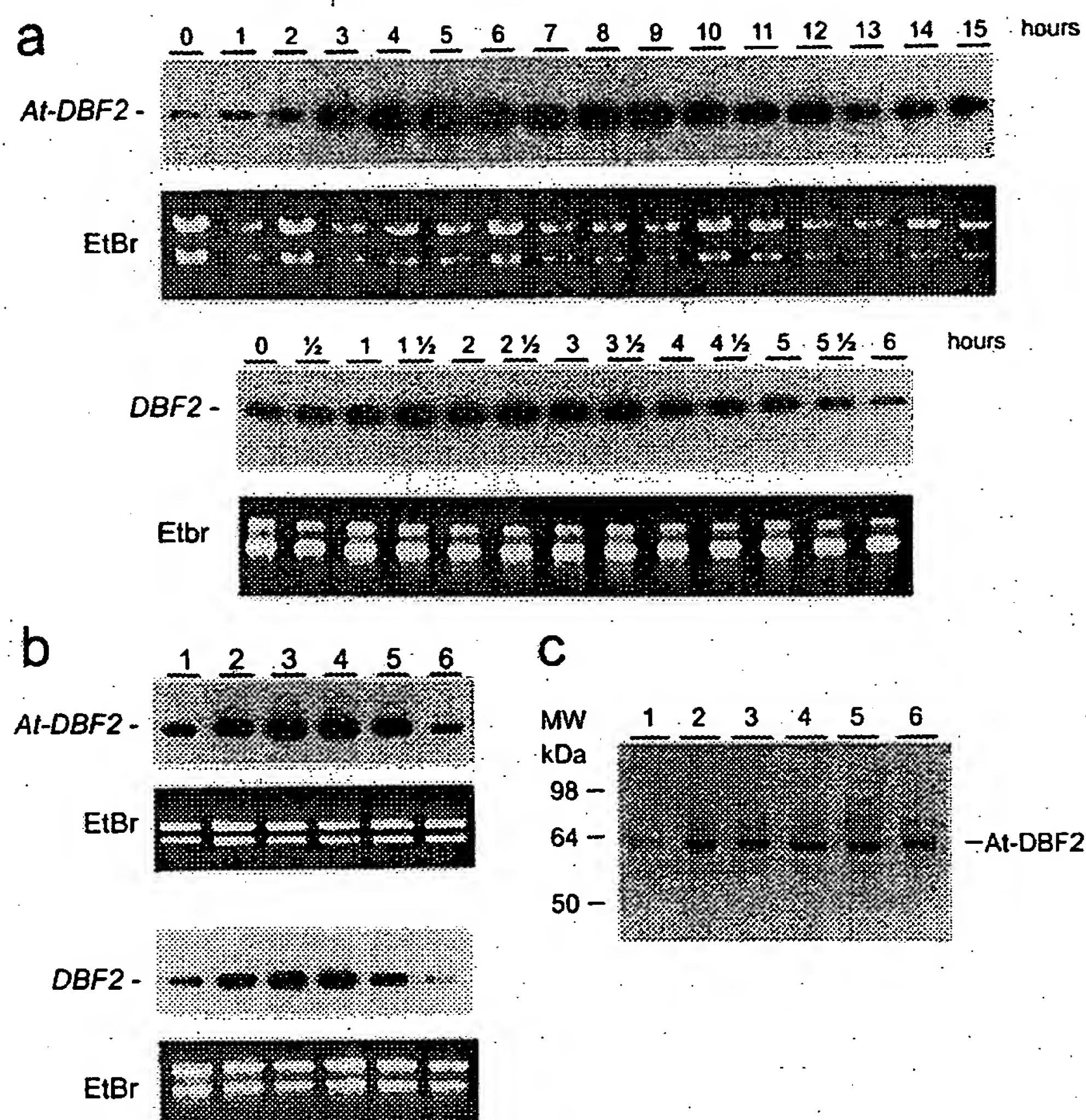


FIGURE 3



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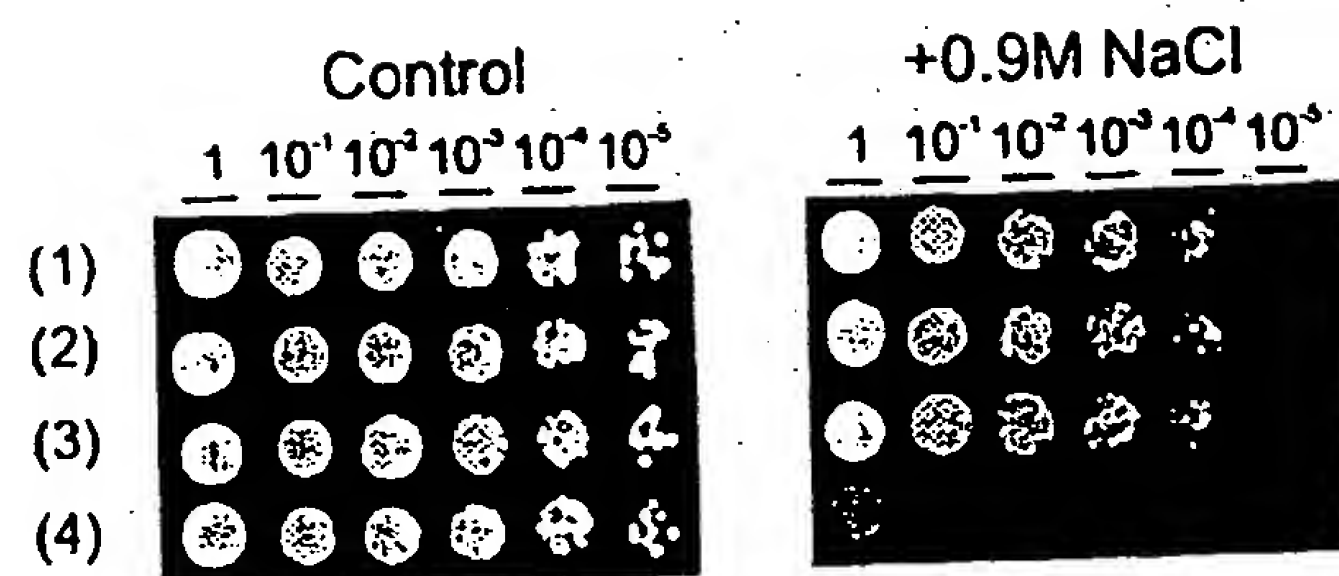


FIGURE 4

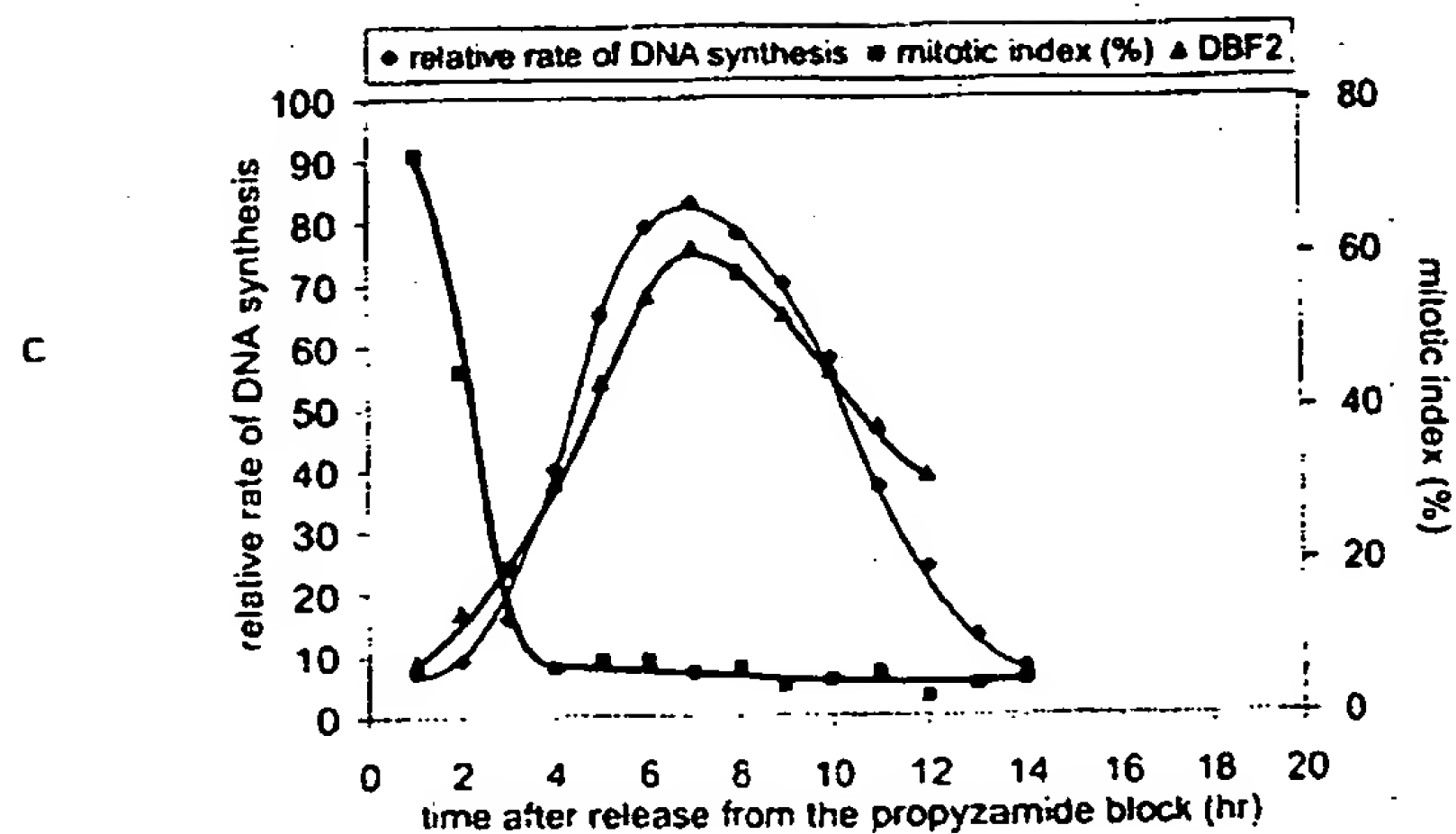
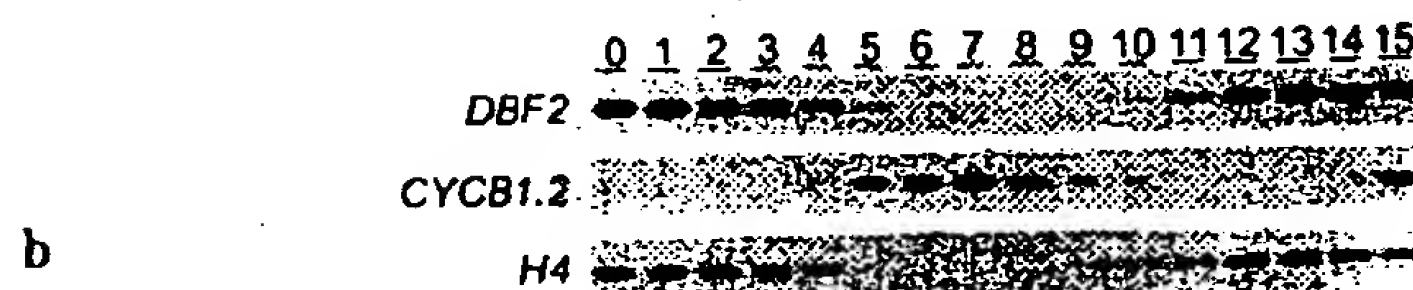
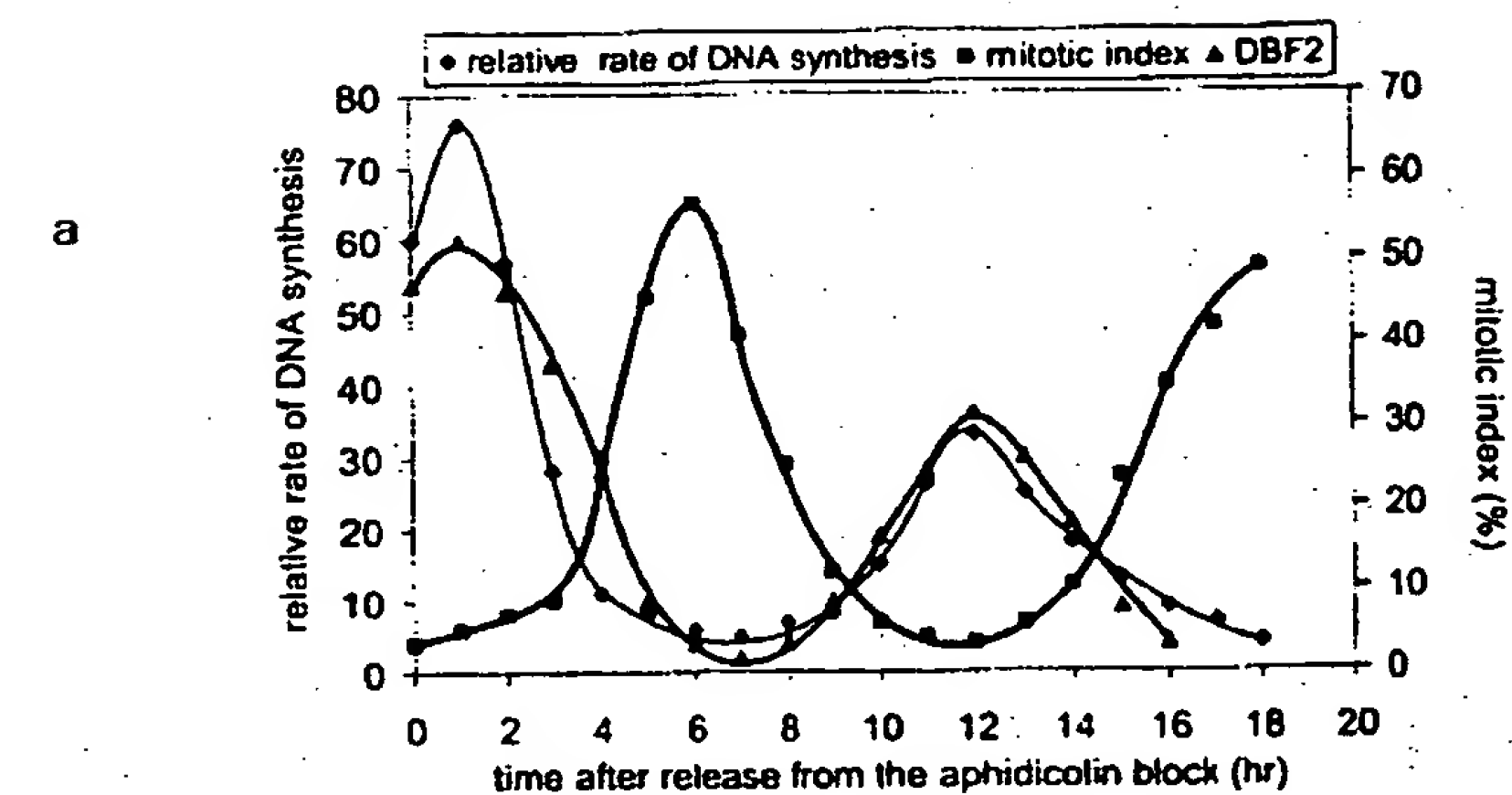


FIGURE 5

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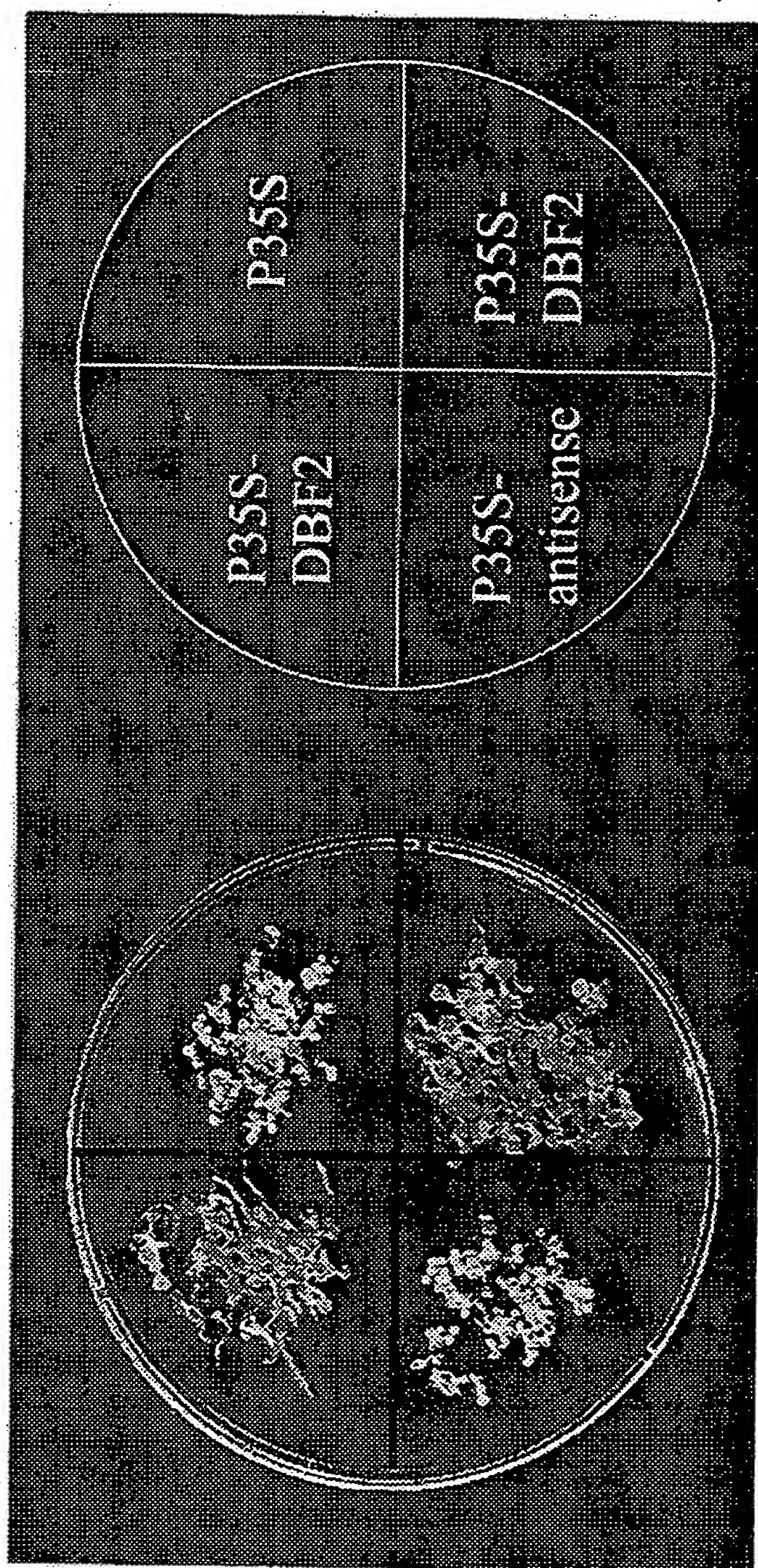


FIGURE 6

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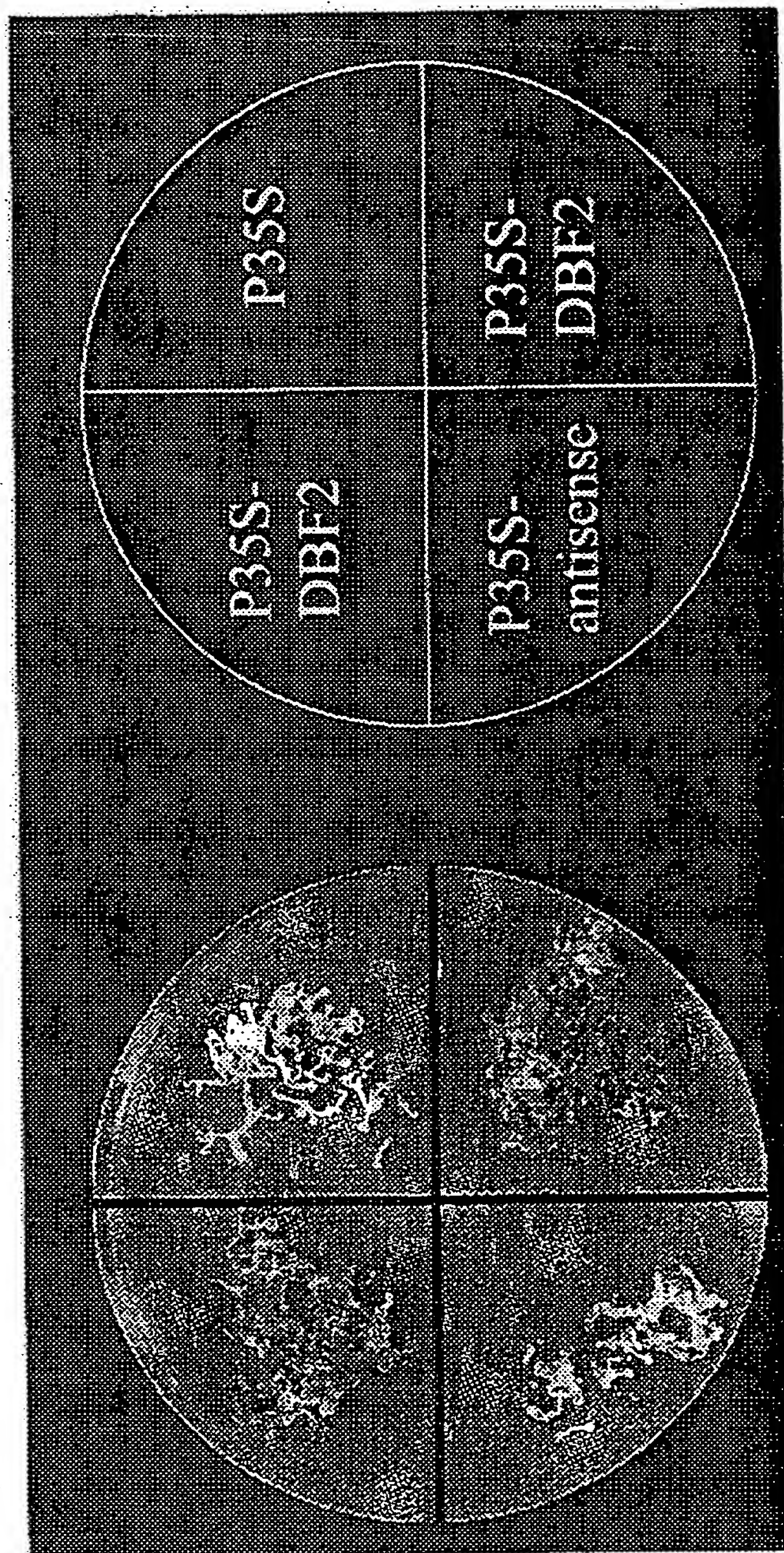


FIGURE 7



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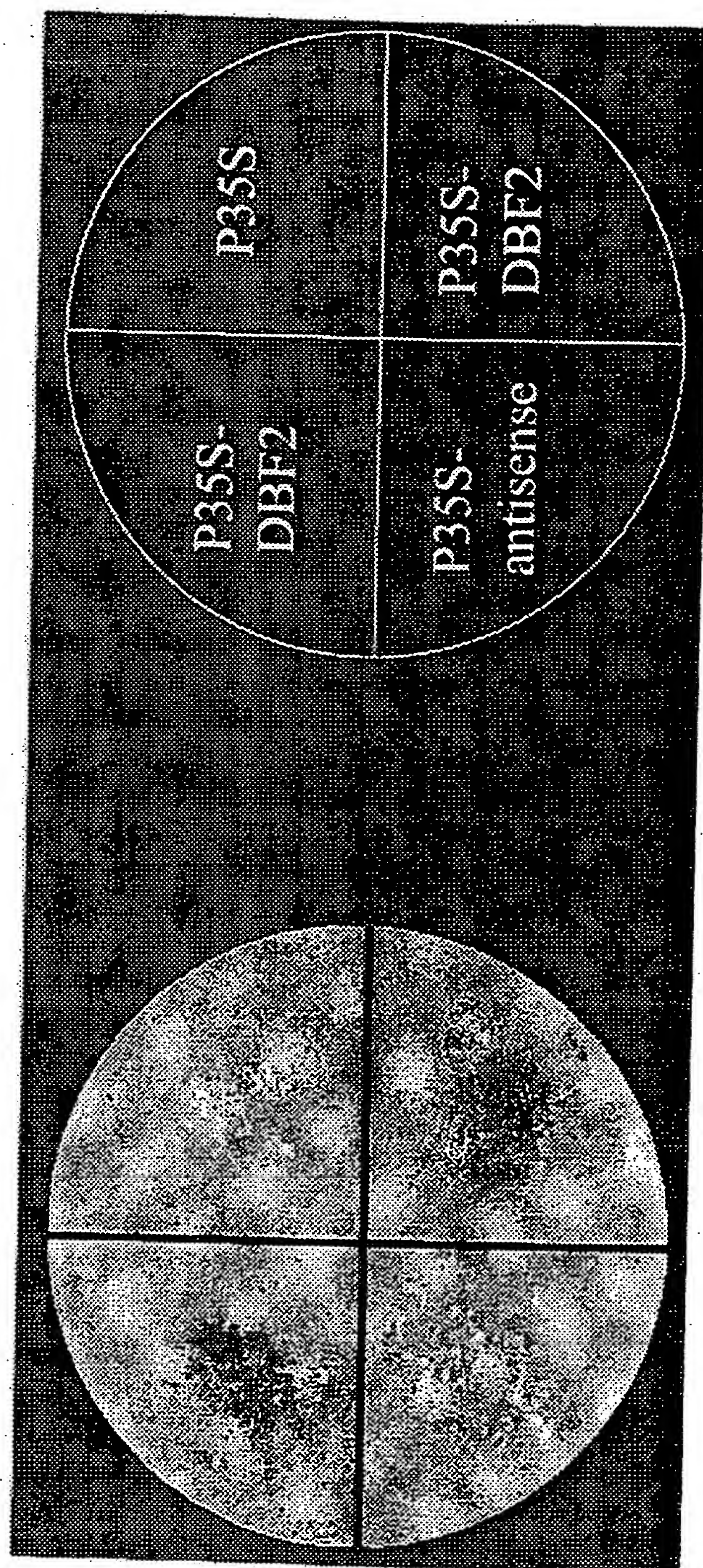


FIGURE 8

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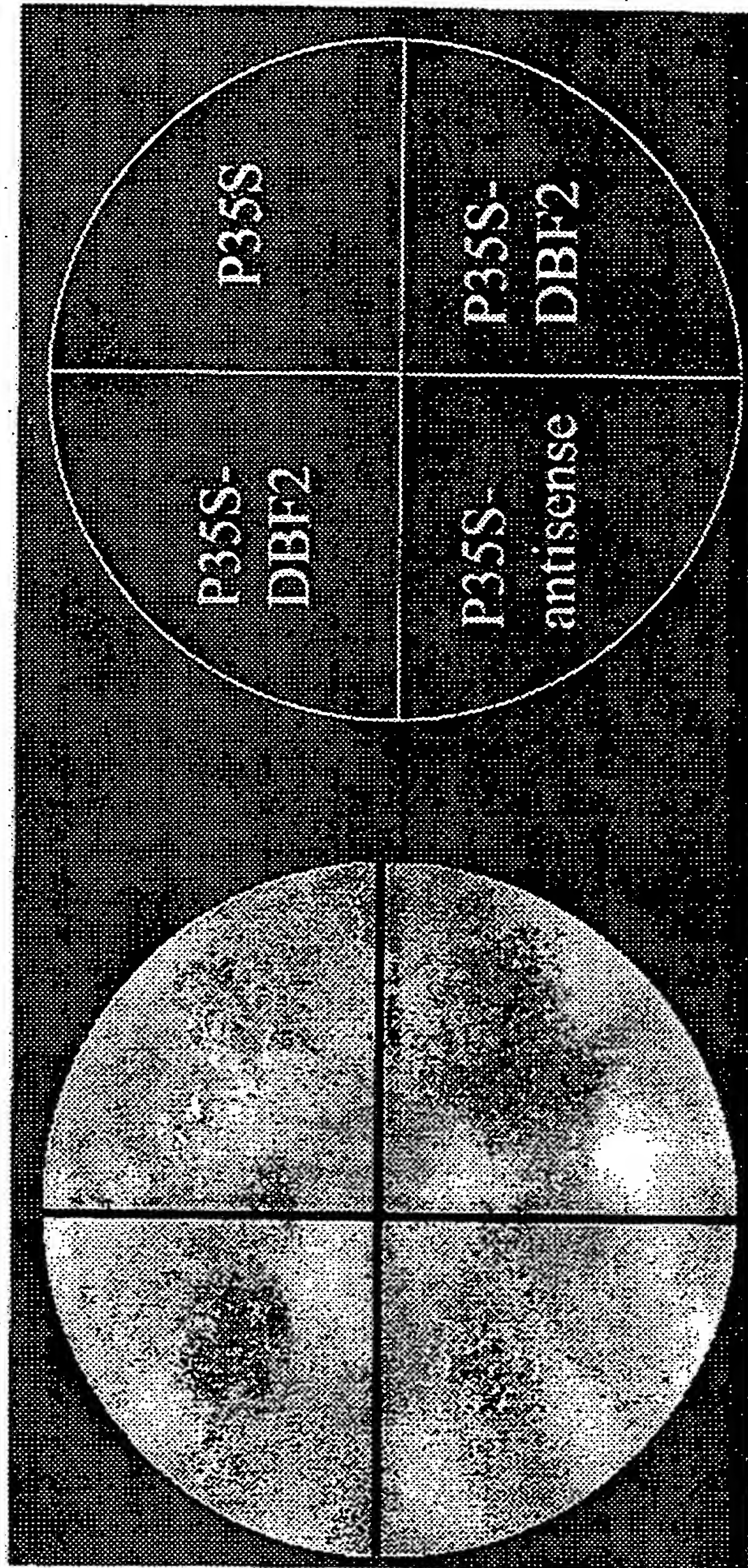


FIGURE 9



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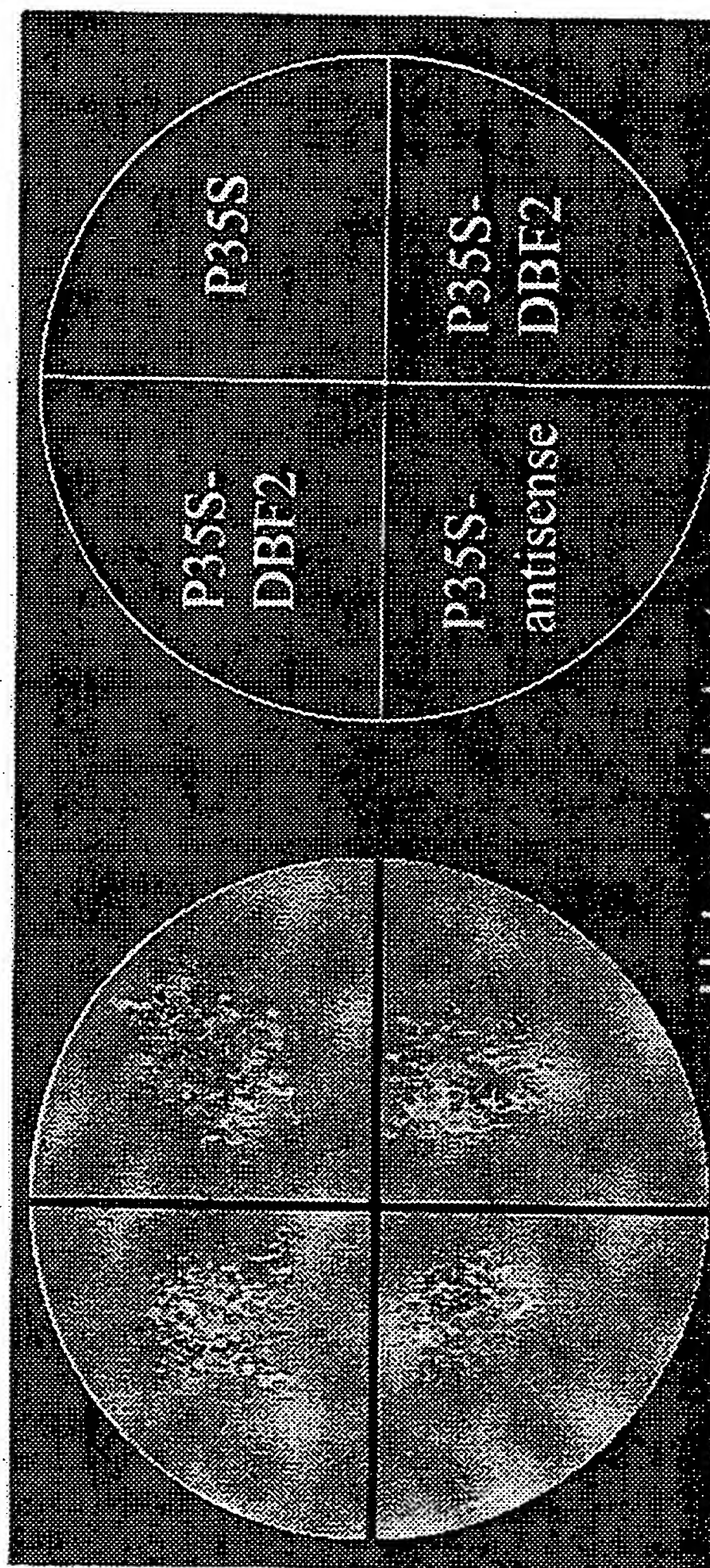


FIGURE 10

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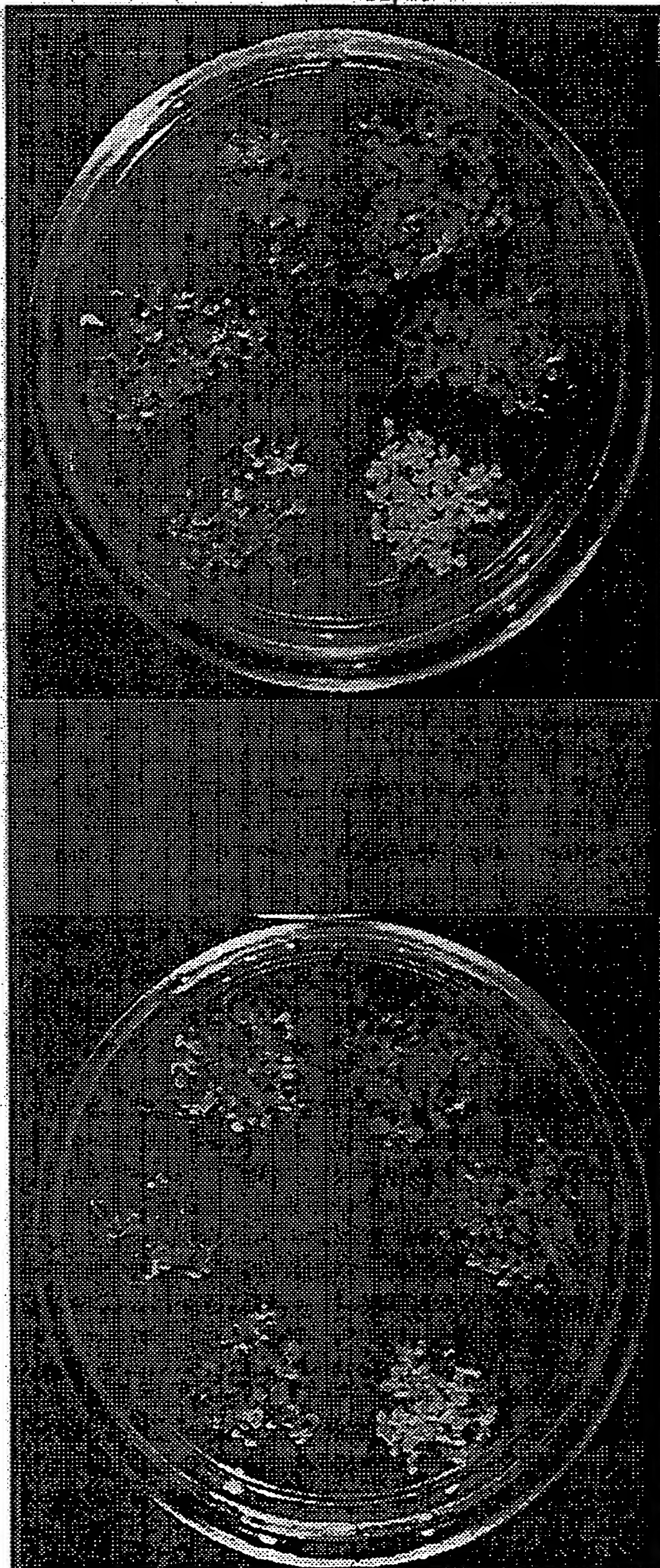


FIGURE 11



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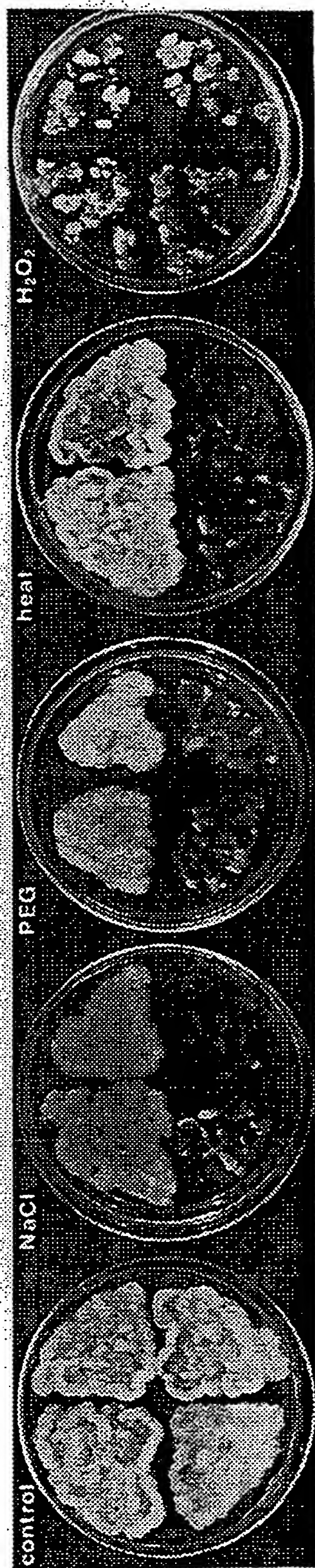


FIGURE 12A

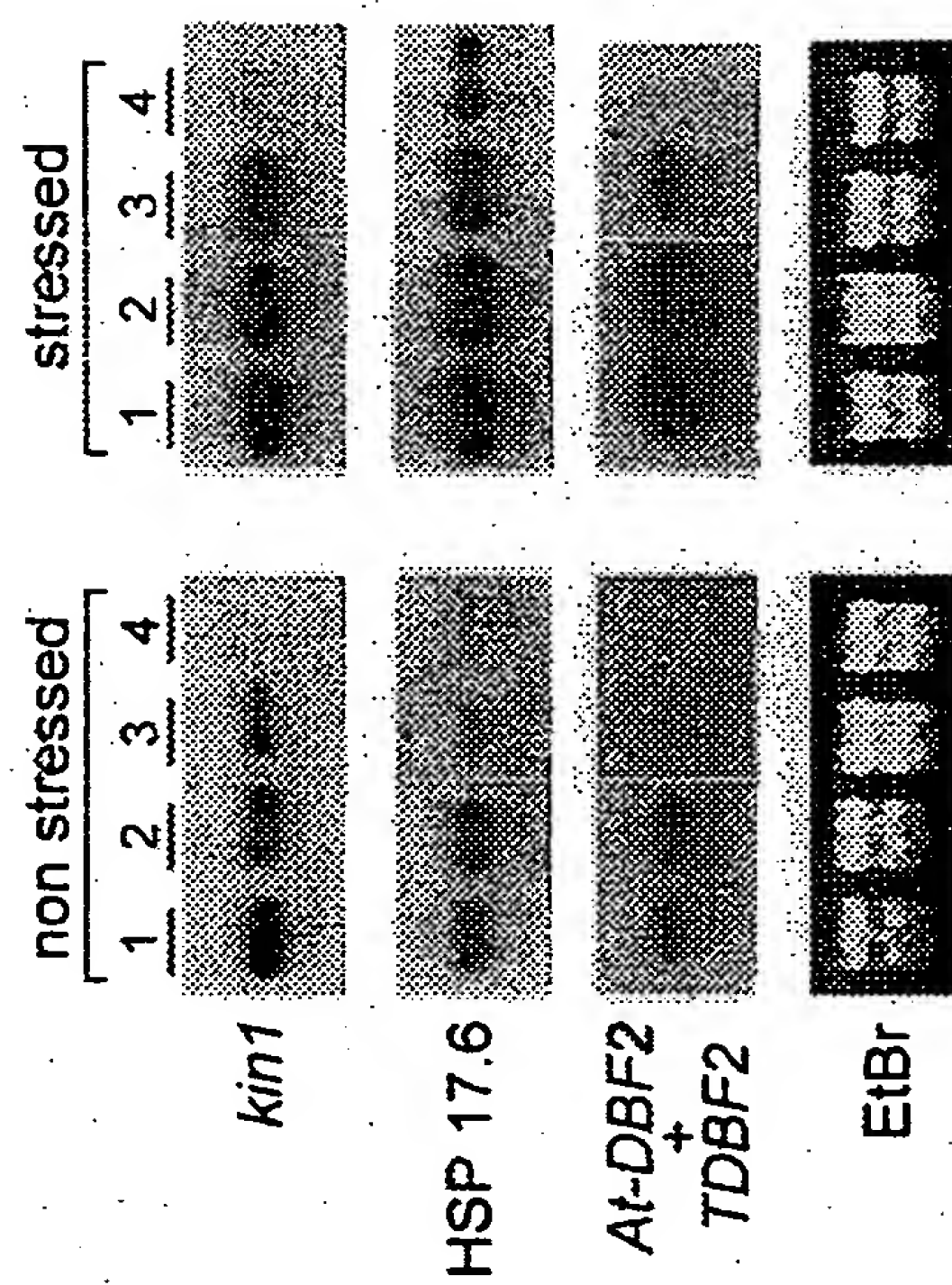


FIGURE 12c

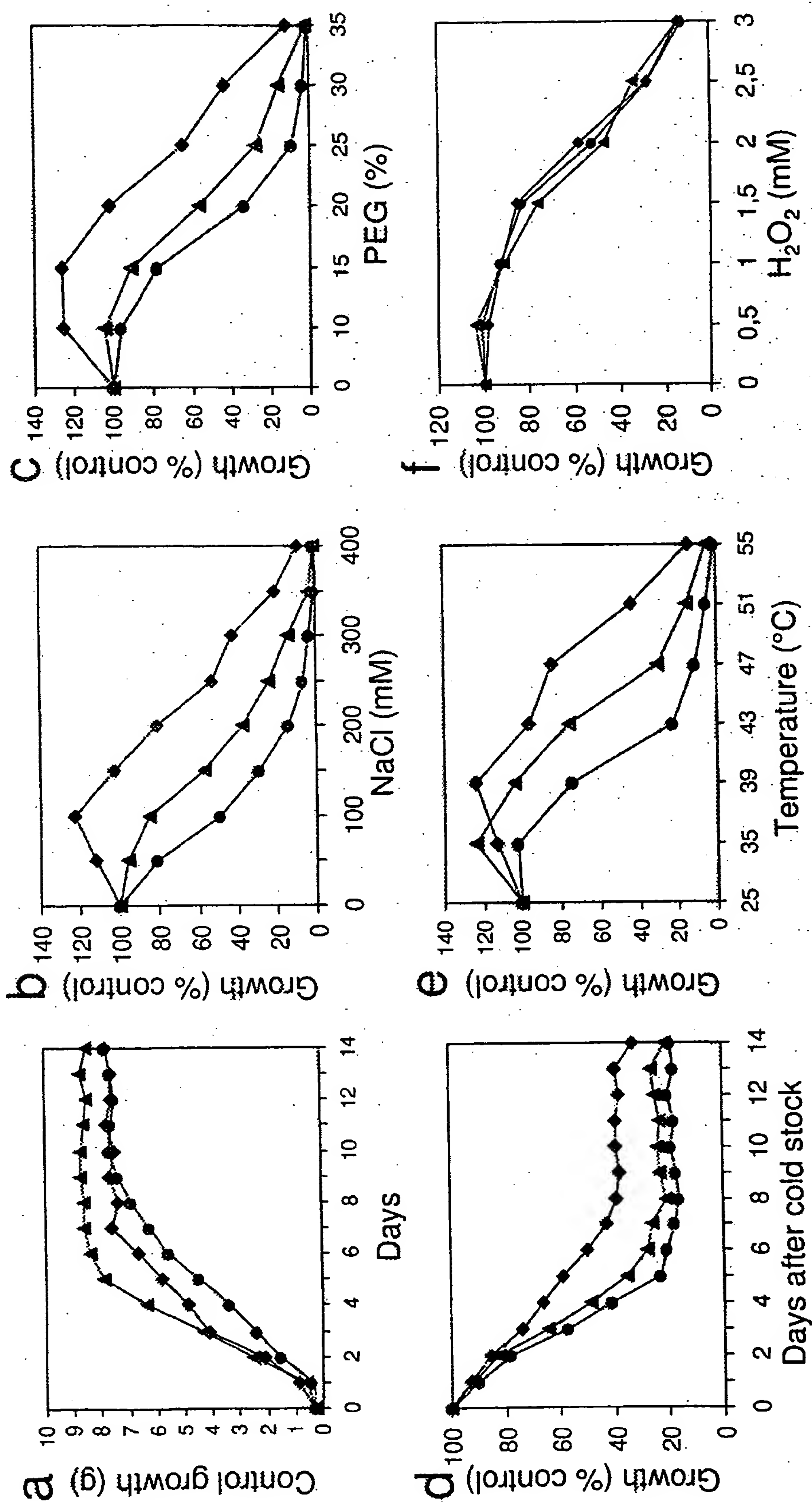


FIGURE 12B



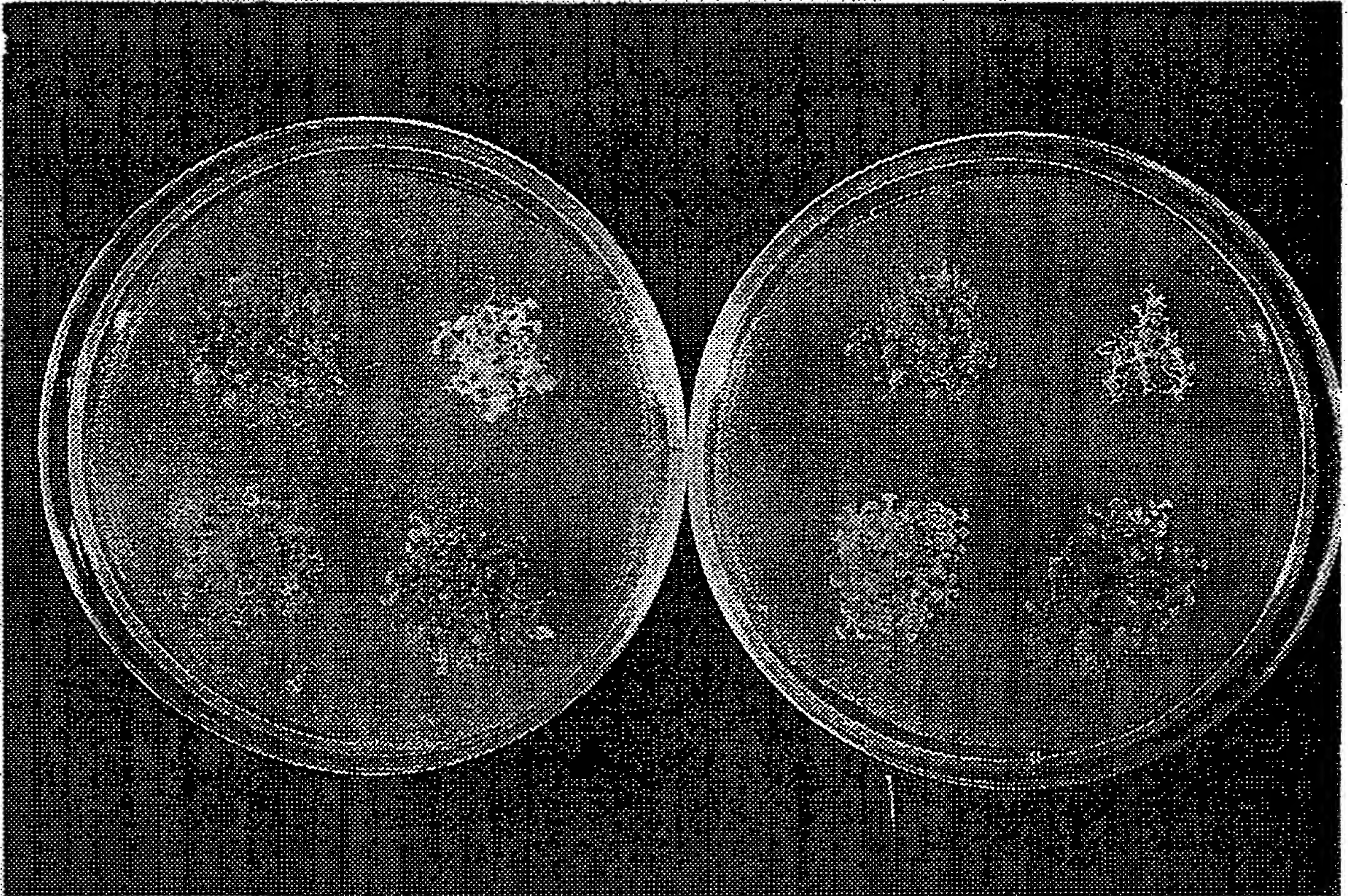


FIGURE 13



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FIGURE 14

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Pro Thr Lys Tyr Ser Ser Asn Ser Pro Pro Val Ser Pro Ala Ile Phe  
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Tyr Glu Arg Ala Thr Ser Trp Cys Thr Gln Arg Val Val Ser Gly Arg  
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Ala Met Tyr Phe Leu Glu Tyr Tyr Cys Asp Met Phe Asp Tyr Val Ile  
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Ser Arg Arg Gln Arg Thr Lys Gln Val Leu Glu Tyr Leu Gln Gln Gln  
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Ser Gln Leu Pro Asn Ser Asp Gln Ile Lys Leu Asn Glu Glu Trp Ser  
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Ser Tyr Leu Gln Arg Glu His Gln Val Leu Ser Lys Arg Arg Leu Lys  
145 150 155 160

Pro Lys Asn Arg Asp Phe Glu Met Ile Thr Gln Val Gly Gln Gly Gly  
165 170 175

Tyr Gly His Val Tyr Leu Ala Arg Lys Lys Asp Thr Lys Glu Val Cys  
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Ala Leu Lys Ile Leu Asn Lys Lys Leu Gly Phe Lys Leu Asn Gly Thr  
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Cys His Val Leu Thr Glu Arg Gln Ser Leu Thr Thr Thr Arg Ser Glu  
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Gly Arg Arg Cys Leu Lys Ser Gly His Ala Arg Phe Tyr Ile Ser Glu  
 260 265 270  
 Met Phe Cys Ala Val Asn Glu Lys His Leu Leu Ser Lys Thr Asp Ser  
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&lt;221&gt; CDS

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Met Asp Leu Glu Phe Gly Arg  
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Phe Pro Ile Phe Ser Ile Leu Glu Asp Met Leu Glu Ala Pro Glu Glu  
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Gln Thr Glu Lys Thr Arg Asn Asn Pro Ser Arg Ala Tyr Met Arg Asp  
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Ala Lys Ala Met Ala Ala Thr Pro Ala Asp Val Ile Glu His Pro Asp  
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Ala Tyr Val Phe Ala Val Asp Met Pro Gly Ile Lys Gly Asp Glu Ile  
60 65 70cag gtc cag ata gag aac gag aac gtg ctt gtg gtg agt ggc aaa aga 354  
Gln Val Gln Ile Glu Asn Glu Asn Val Leu Val Val Ser Gly Lys Arg  
75 80 85cag agg gac aac aag gag aat gaa ggt gtg aag ttt gtg agg atg gag 402  
Gln Arg Asp Asn Lys Glu Asn Glu Gly Val Lys Phe Val Arg Met Glu  
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Arg Arg Met Gly Lys Phe Met Arg Lys Phe Gln Leu Pro Asp Asn Ala  
105 110 115gat ttg gag aag atc tct gcg gct tgt aat gac ggt gtg ttg aaa gtg 498  
Asp Leu Glu Lys Ile Ser Ala Ala Cys Asn Asp Gly Val Leu Lys Val  
120 125 130 135act att ccg aaa ctt cct cct cct gag cca aag aaa cca aag act ata 546  
Thr Ile Pro Lys Leu Pro Pro Pro Glu Pro Lys Lys Pro Lys Thr Ile  
140 145 150caa gtt caa gtc gct tga gtttggttgt gatccgtgtt tttgtgtttt 594  
Gln Val Gln Val Ala  
155

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 Ser Arg Ala Tyr Met Arg Asp Ala Lys Ala Met Ala Ala Thr Pro Ala  
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 Val Lys Phe Val Arg Met Glu Arg Arg Met Gly Lys Phe Met Arg Lys  
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 Phe Gln Leu Pro Asp Asn Ala Asp Leu Glu Lys Ile Ser Ala Ala Cys  
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 Asn Asp Gly Val Leu Lys Val Thr Ile Pro Lys Leu Pro Pro Pro Glu  
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Leu Val Arg His Gly Glu Ser Glu Gly Asn Leu Asp Thr Ala Ala Tyr	
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aca acg acg ccg gat cat aag atc cag tta acg gat tcc ggt ttg ctt	267
Thr Thr Thr Pro Asp His Lys Ile Gln Leu Thr Asp Ser Gly Leu Leu	
30 35 40 45	
cag gcg cag gaa gcc gga gct cgt ctc cac gct ttg atc tct tct aat	315
Gln Ala Gln Glu Ala Gly Ala Arg Leu His Ala Leu Ile Ser Ser Asn	
50 55 60	
cct tct tca ccg gag tgg cgt gtg tac ttc tac gtt tcg ccg tac gat	363
Pro Ser Ser Pro Glu Trp Arg Val Tyr Phe Tyr Val Ser Pro Tyr Asp	
65 70 75	
cgg act cga tct acg ctc cgg gag atc gga cgg tcg ttc tcg cgt cgc	411
Arg Thr Arg Ser Thr Leu Arg Glu Ile Gly Arg Ser Phe Ser Arg Arg	
80 85 90	
cgt gtg att ggt gtt cgc gaa gaa tgt cgg att agg gaa cag gat ttt	459
Arg Val Ile Gly Val Arg Glu Glu Cys Arg Ile Arg Glu Gln Asp Phe	
95 100 105	
ggg aat ttt cag gtt aaa gag cga atg aga gca acg aaa aag gtc aga	507
Gly Asn Phe Gln Val Lys Glu Arg Met Arg Ala Thr Lys Lys Val Arg	
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Glu Arg Phe Gly Arg Phe Phe Tyr Arg Phe Pro Glu Gly Glu Ser Ala	
130 135 140	
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Ala Asp Val Phe Asp Arg Val Ser Ser Phe Leu Glu Ser Leu Trp Arg	
145 150 155	
gac att gac atg aac aga ctg cac atc aac ccg tct cat gag cta aac	651
Asp Ile Asp Met Asn Arg Leu His Ile Asn Pro Ser His Glu Leu Asn	
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ttt gtg att gtc tca cat ggc tta aca tcg cgt gtg ttt ctg atg aaa	699
Phe Val Ile Val Ser His Gly Leu Thr Ser Arg Val Phe Leu Met Lys	
175 180 185	
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Trp Phe Lys Trp Ser Val Glu Gln Phe Glu Gly Leu Asn Asn Pro Gly	
190 195 200 205	
aac agt gag atc aga gtg atg gaa tta gga caa ggc ggt gat tac agc	795
Asn Ser Glu Ile Arg Val Met Glu Leu Gly Gln Gly Gly Asp Tyr Ser	
210 215 220	
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Leu Ala Ile His His Thr Glu Glu Glu Leu Ala Thr Trp Gly Leu Ser	
225 230 235	
cca gag atg att gca gat caa aag tgg cgg gct aac gcg cat aaa ggc	891

Pro Glu Met Ile Ala Asp Gln Lys Trp Arg Ala Asn Ala His Lys Gly  
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gaa tgg aaa gaa gat tgt aag tgg tat ttt ggt gat ttc ttc gac cat 939  
 Glu Trp Lys Glu Asp Cys Lys Trp Tyr Phe Gly Asp Phe Phe Asp His  
 255 260 265

atg gca gat tcc gat aaa gag tgc gag act gag gcc act gaa gat aga 987  
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 270 275 280 285

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 35 40 45

Glu Ala Gly Ala Arg Leu His Ala Leu Ile Ser Ser Asn Pro Ser Ser  
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Pro Glu Trp Arg Val Tyr Phe Tyr Val Ser Pro Tyr Asp Arg Thr Arg  
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Ser Thr Leu Arg Glu Ile Gly Arg Ser Phe Ser Arg Arg Arg Val Ile  
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Gly Val Arg Glu Glu Cys Arg Ile Arg Glu Gln Asp Phe Gly Asn Phe  
 100 105 110

Gln Val Lys Glu Arg Met Arg Ala Thr Lys Lys Val Arg Glu Arg Phe  
 115 120 125



Gly Arg Phe Phe Tyr Arg Phe Pro Glu Gly Glu Ser Ala Ala Asp Val  
 130 135 140  
 Phe Asp Arg Val Ser Ser Phe Leu Glu Ser Leu Trp Arg Asp Ile Asp  
 145 150 155 160  
 Met Asn Arg Leu His Ile Asn Pro Ser His Glu Leu Asn Phe Val Ile  
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 Val Ser His Gly Leu Thr Ser Arg Val Phe Leu Met Lys Trp Phe Lys  
 180 185 190  
 Trp Ser Val Glu Gln Phe Glu Gly Leu Asn Asn Pro Gly Asn Ser Glu  
 195 200 205  
 Ile Arg Val Met Glu Leu Gly Gln Gly Gly Asp Tyr Ser Leu Ala Ile  
 210 215 220  
 His His Thr Glu Glu Glu Leu Ala Thr Trp Gly Leu Ser Pro Glu Met  
 225 230 235 240  
 Ile Ala Asp Gln Lys Trp Arg Ala Asn Ala His Lys Gly Glu Trp Lys  
 245 250 255  
 Glu Asp Cys Lys Trp Tyr Phe Gly Asp Phe Phe Asp His Met Ala Asp  
 260 265 270  
 Ser Asp Lys Glu Cys Glu Thr Glu Ala Thr Glu Asp Arg Glu Glu Glu  
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 Val Ala Ile Ile Thr Gly Gly Ala Arg Gly Ile Gly Ala Ala Thr Ala  
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aga ttg ttc aca gag aat ggc gcg tat gtg ata gtc gcg gat atc ctt	147
Arg Leu Phe Thr Glu Asn Gly Ala Tyr Val Ile Val Ala Asp Ile Leu	
30 35 40	
gat aat gaa ggc atc ctt gtg gcg gaa tcg atc ggt ggg tgt tac gtt	195
Asp Asn Glu Gly Ile Leu Val Ala Glu Ser Ile Gly Gly Cys Tyr Val	
45 50 55	
cat tgt gac gta tcg aag gag gct gat gtt gag gcg gca gtg gag cta	243
His Cys Asp Val Ser Lys Glu Ala Asp Val Glu Ala Ala Val Glu Leu	
60 65 70 75	
gca atg aga cgt aaa ggt aga cta gat gtg atg ttc aac aat gcc ggg	291
Ala Met Arg Arg Lys Gly Arg Leu Asp Val Met Phe Asn Asn Ala Gly	
80 85 90	
atg tcg ctt aac gaa ggt agt atc atg ggg atg gac gtg gac atg gtt	339
Met Ser Leu Asn Glu Gly Ser Ile Met Gly Met Asp Val Asp Met Val	
95 100 105	
aac aaa ctt gtc tcg gtt aat gtc aat ggt gtt ttg cat ggt atc aaa	387
Asn Lys Leu Val Ser Val Asn Val Asn Gly Val Leu His Gly Ile Lys	
110 115 120	
cat gcc gct aag gcc atg atc aaa ggg gga cga gga ggc tcg ata ata	435
His Ala Ala Lys Ala Met Ile Lys Gly Gly Arg Gly Gly Ser Ile Ile	
125 130 135	
tgc aca tcg agc tca tca ggg cta atg gga gga ctt gga gga cat gcg	483
Cys Thr Ser Ser Ser Ser Gly Leu Met Gly Gly Leu Gly Gly His Ala	
140 145 150 155	
tat acg ctc tcc aaa gga ggc atc aac ggg gtg gtg agg aca acg gag	531
Tyr Thr Leu Ser Lys Gly Gly Ile Asn Gly Val Val Arg Thr Thr Glu	
160 165 170	
tgc gag ctt ggg tct cac ggc atc cgt gtg aat agc atc tct cct cat	579
Cys Glu Leu Gly Ser His Gly Ile Arg Val Asn Ser Ile Ser Pro His	
175 180 185	
gga gtt ccc act gac atc ttg gtt aat gcg tac cgt aag ttc ctt aac	627
Gly Val Pro Thr Asp Ile Leu Val Asn Ala Tyr Arg Lys Phe Leu Asn	
190 195 200	
aat gac aaa ctc aac gtc gct gag gtc acc gac att att gct gag aaa	675
Asn Asp Lys Leu Asn Val Ala Glu Val Thr Asp Ile Ile Ala Glu Lys	
205 210 215	
ggg agt ttg ctg acc gga aga gcc ggt act gtg gag gac gta gct caa	723
Gly Ser Leu Leu Thr Gly Arg Ala Gly Thr Val Glu Asp Val Ala Gln	
220 225 230 235	
gca gct ttg ttt ctt gca agc caa gaa tcg tcg ggg ttc att acc gga	771
Ala Ala Leu Phe Leu Ala Ser Gln Glu Ser Ser Gly Phe Ile Thr Gly	
240 245 250	
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His Asn Leu Val Val Asp Gly Gly Tyr Thr Ser Ala Thr Ser Thr Met  
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aga ttt atc tac aac tag ttttcgtttg gtggtgtttc cttttc  
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863

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Asn Gly Ala Tyr Val Ile Val Ala Asp Ile Leu Asp Asn Glu Gly Ile  
 35 40 45

Leu Val Ala Glu Ser Ile Gly Gly Cys Tyr Val His Cys Asp Val Ser  
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Lys Glu Ala Asp Val Glu Ala Ala Val Glu Leu Ala Met Arg Arg Lys  
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Gly Arg Leu Asp Val Met Phe Asn Asn Ala Gly Met Ser Leu Asn Glu  
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Gly Ser Ile Met Gly Met Asp Val Asp Met Val Asn Lys Leu Val Ser  
 100 105 110

Val Asn Val Asn Gly Val Leu His Gly Ile Lys His Ala Ala Lys Ala  
 115 120 125

Met Ile Lys Gly Gly Arg Gly Gly Ser Ile Ile Cys Thr Ser Ser Ser  
 130 135 140

Ser Gly Leu Met Gly Gly Leu Gly Gly His Ala Tyr Thr Leu Ser Lys  
 145 150 155 160

Gly Gly Ile Asn Gly Val Val Arg Thr Thr Glu Cys Glu Leu Gly Ser  
 165 170 175

His Gly Ile Arg Val Asn Ser Ile Ser Pro His Gly Val Pro Thr Asp  
 180 185 190

Ile Leu Val Asn Ala Tyr Arg Lys Phe Leu Asn Asn Asp Lys Leu Asn  
 195 200 205

Val Ala Glu Val Thr Asp Ile Ile Ala Glu Lys Gly Ser Leu Leu Thr  
 210 215 220

Gly Arg Ala Gly Thr Val Glu Asp Val Ala Gln Ala Ala Leu Phe Leu

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 Tyr Arg Pro Ser Ser Ala Tyr Asn Ala Pro Phe Tyr Thr Thr Asn  
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 Phe Phe Glu Val Thr His Asp Ile Ser Asn Leu Thr Cys Ala Asp Phe  
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 Val Val His Gly Arg Ala Ser Pro Glu Thr Met Arg Asp Ile Arg Gly  
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 135 140

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 Phe Ile Arg Asp Gly Ile Gln Phe Pro Asp Val Val His Ala Leu Lys  
 145 150 155

cct aac cga aaa aca aac atc caa gag tac tgg agg att ctg gac tac 1712  
 Pro Asn Arg Lys Thr Asn Ile Gln Glu Tyr Trp Arg Ile Leu Asp Tyr  
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 180 185 190

gat gtt ggt att cca caa gat tac agg cat atg gag ggt ttc ggt gtc 1808  
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 195 200 205

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 210 215 220

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 225 230 235

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 240 245 250 255

cac gat gcc att gca tct ggc aac tac ccc gag tgg aaa ctt ttc atc 2000  
 His Asp Ala Ile Ala Ser Gly Asn Tyr Pro Glu Trp Lys Leu Phe Ile  
 260 265 270

cag acc atg gat cct gca gat gag gat aag ttt gac ttt gac cca ctt 2048  
 Gln Thr Met Asp Pro Ala Asp Glu Asp Lys Phe Asp Phe Asp Pro Leu  
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Ser Asp Asp Lys Leu Leu Gln Cys Arg Ile Phe Ala Tyr Gly Asp Thr	340	345	350	
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Pro Lys Cys Ala His His Asn Asn His His Glu Gly Phe Met Asn Phe	370	375	380	
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			Ile	
			390	
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Asn Tyr Tyr Pro Ser Lys Phe Asp Pro Val Arg Cys Ala Glu Lys Val	395	400	405	
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Pro Thr Pro Thr Asn Ser Tyr Thr Gly Ile Arg Thr Lys	410	415		
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Asp Arg Phe Val Lys Arg Trp Val Glu Ile Leu Ser Glu Pro Arg Leu	445	450	455	
acc cac gag atc cgc ggc atc tgg acc tct tac tgg ctc aag				2790
Thr His Glu Ile Arg Gly Ile Trp Thr Ser Tyr Trp Leu Lys	460	465	470	
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Lys Leu Ala Ser Arg Leu Asn Val Arg Pro Ser Ile	485	490		

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 Ile Arg Thr Lys Cys Val Ile Lys Lys Glu Asn Asn Phe Lys Gln Ala  
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Lys Ser Lys Leu Asp Gly Gln Pro Glu Leu Phe Ile Arg Leu Val Pro
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gac aag cct aat aag acg ctc tca att att gac agt ggt att ggc atg      652
Asp Lys Pro Asn Lys Thr Leu Ser Ile Ile Asp Ser Gly Ile Gly Met
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Lys Ile Ser Leu Phe Leu Lys Asp Asp Gln  
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Val Lys Lys Cys Ile Glu Met Phe Asn Glu Ile Ala Glu Asn Lys Glu	
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Tyr His Ser Thr Lys Ser Gly Asp Glu Met Thr Ser Phe Lys Asp Tyr	
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Val Thr Arg Met Lys Glu Gly Gln Lys Asp Ile Phe Tyr Ile Thr Gly	
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 Lys His Asn Asp Asp Glu Gln Tyr Val Trp Glu Ser Gln Ala Gly Gly  
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Asp Lys Leu Val Glu Tyr Asp Ala Leu Leu Leu Asp Arg Phe Leu Asp  
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45 50 55

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80 85 90

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Ile Val Ile Ser Lys Ala Phe Ser His Met Leu Asn Leu Ala Asn Leu  
95 100 105

gct gag gag gtg cag att gct cac cgt cgc agg atc aag aag ctg aag 386  
Ala Glu Glu Val Gln Ile Ala His Arg Arg Arg Ile Lys Lys Leu Lys

110	115	120	
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gaa gag act ttt aag agg ctc gtt tcg gat ctt ggt aag tct cct gaa Glu Glu Thr Phe Lys Arg Leu Val Ser Asp Leu Gly Lys Ser Pro Glu 140 145 150 155			482
gag atc ttt gat gcc ttg aag aat cag act gtg gat ctg gtt ttg act Glu Ile Phe Asp Ala Leu Lys Asn Gln Thr Val Asp Leu Val Leu Thr 160 165 170			530
gct cat cct act cag tct gtg cgt aga tca ttg ctt cag aag cat ggg Ala His Pro Thr Gln Ser Val Arg Arg Ser Leu Leu Gln Lys His Gly 175 180 185			578
agg ata agg gac tgt ctt gct caa ctc tat gca aag gac att act cct Arg Ile Arg Asp Cys Leu Ala Gln Leu Tyr Ala Lys Asp Ile Thr Pro 190 195 200			626
gat gac aag cag gag cta gat gag tct ctg caa aga gag att caa gct Asp Asp Lys Gln Glu Leu Asp Glu Ser Leu Gln Arg Glu Ile Gln Ala 205 210 215			674
gca ttc cga aca gat gag att aga aga aca cct cca acc cca caa gat Ala Phe Arg Thr Asp Glu Ile Arg Arg Thr Pro Pro Thr Pro Gln Asp 220 225 230 235			722
gaa atg aga gct gga atg agt tat ttc cac gag aca atc tgg aaa ggt Glu Met Arg Ala Gly Met Ser Tyr Phe His Glu Thr Ile Trp Lys Gly 240 245 250			770
gtc ccc aag ttc ttg cgc cgt gtg gac aca gct ctg aaa aac att ggg Val Pro Lys Phe Leu Arg Arg Val Asp Thr Ala Leu Lys Asn Ile Gly 255 260 265			818
att gat gaa cgt gtt cct tac aat gcc cca ttg att caa ttc tct tcg Ile Asp Glu Arg Val Pro Tyr Asn Ala Pro Leu Ile Gln Phe Ser Ser 270 275 280			866
tgg atg ggc ggt gat cgt gat ggt aat ccg agg gtc aca cct gag gtc Trp Met Gly Gly Asp Arg Asp Gly Asn Pro Arg Val Thr Pro Glu Val 285 290 295			914
act aga gat gtg tgc ttg ttg gct aga atg atg gct gcc aat ctc tac Thr Arg Asp Val Cys Leu Leu Ala Arg Met Met Ala Ala Asn Leu Tyr 300 305 310 315			962
tat aac caa atc gag aat ctg atg ttt gag tta tct atg tgg cgt tgc Tyr Asn Gln Ile Glu Asn Leu Met Phe Glu Leu Ser Met Trp Arg Cys 320 325 330			1010
act gat gaa ttc cgt gtg cgg gcg gat gaa ctg cac agg aac tca agg Thr Asp Glu Phe Arg Val Arg Ala Asp Glu Leu His Arg Asn Ser Arg 335 340 345			1058

aaa gat gct gca aaa cat tac ata gaa ttc tgg aag aca att cct cca	1106
Lys Asp Ala Ala Lys His Tyr Ile Glu Phe Trp Lys Thr Ile Pro Pro	
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act gag cca tac cgt gtg att ctt ggt gat gtg agg gat aag ctg tat	1154
Thr Glu Pro Tyr Arg Val Ile Leu Gly Asp Val Arg Asp Lys Leu Tyr	
365 370 375	
cac aca cgt gag cgt tcc cgc caa ttg ctg agt aat gga atc tcg gat	1202
His Thr Arg Glu Arg Ser Arg Gln Leu Leu Ser Asn Gly Ile Ser Asp	
380 385 390 395	
att cct gaa gaa gct acc ttc act aat gtg gaa cag ttc ttg gag cct	1250
Ile Pro Glu Glu Ala Thr Phe Thr Asn Val Glu Gln Phe Leu Glu Pro	
400 405 410	
ctt gag ctc tgt tac cga tca cta tgt tca tgt ggt gac agc ccg ata	1298
Leu Glu Leu Cys Tyr Arg Ser Leu Cys Ser Cys Gly Asp Ser Pro Ile	
415 420 425	
gct gat gga agc ctt ctt gat ttc ttg agg caa gtc tct acc ttt gga	1346
Ala Asp Gly Ser Leu Leu Asp Phe Leu Arg Gln Val Ser Thr Phe Gly	
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ctc tcc ctt gtg aga ctt gac atc agg caa gag tct gaa cgc cac aca	1394
Leu Ser Leu Val Arg Leu Asp Ile Arg Gln Glu Ser Glu Arg His Thr	
445 450 455	
gat gtc ttg gat gct atc acc aag cac ttg gac atc ggt tcc tcc tat	1442
Asp Val Leu Asp Ala Ile Thr Lys His Leu Asp Ile Gly Ser Ser Tyr	
460 465 470 475	
aga gac tgg tct gaa gaa ggc cga cag gaa tgg ctt ctt gct gaa cta	1490
Arg Asp Trp Ser Glu Glu Gly Arg Gln Glu Trp Leu Leu Ala Glu Leu	
480 485 490	
agc ggc aaa cgt cca ctt ttc gga cct gat ctt ccc aaa acc gaa gaa	1538
Ser Gly Lys Arg Pro Leu Phe Gly Pro Asp Leu Pro Lys Thr Glu Glu	
495 500 505	
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Ile Ser Asp Val Leu Asp Thr Phe Lys Val Ile Ser Glu Leu Pro Ser	
510 515 520	
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Asp Cys Phe Gly Ala Tyr Ile Ile Ser Met Ala Thr Ser Pro Ser Asp	
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gtg ctt gcg gtt gag ctt tta cag cgc gaa tgc cat gtg aaa aat cca	1682
Val Leu Ala Val Glu Leu Leu Gln Arg Glu Cys His Val Lys Asn Pro	
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ctt aga gtt gtt cca ctc ttt gag aag cta gct gat ctt gaa gca gct	1730
Leu Arg Val Val Pro Leu Phe Glu Lys Leu Ala Asp Leu Glu Ala Ala	
560 565 570	

cct gcc gct gtt gca aga ctc ttt tct ata gac tgg tac aaa aac cgt	1778
Pro Ala Ala Val Ala Arg Leu Phe Ser Ile Asp Trp Tyr Lys Asn Arg	
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Ile Asn Gly Lys Gln Glu Val Met Ile Gly Tyr Ser Asp Ser Gly Lys	
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Asp Ala Gly Arg Leu Ser Ala Ala Trp Glu Leu Tyr Lys Ala Gln Glu	
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Glu Leu Val Lys Val Ala Lys Lys Tyr Gly Val Lys Leu Thr Met Phe	
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His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly Gly Pro Thr His Leu	
640 645 650	
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Ala Ile Leu Ser Gln Pro Pro Asp Thr Val Asn Gly Ser Leu Arg Val	
655 660 665	
acg gtt cag ggt gaa gtc att gag caa tca ttt ggg gag gca cac tta	2066
Thr Val Gln Gly Glu Val Ile Glu Gln Ser Phe Gly Glu Ala His Leu	
670 675 680	
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Cys Phe Arg Thr Leu Gln Arg Phe Thr Ala Ala Thr Leu Glu His Gly	
685 690 695	
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Met Asn Pro Pro Ile Ser Pro Lys Pro Glu Trp Arg Ala Leu Leu Asp	
700 705 710 715	
gaa atg gcg gtt gtt gca act gag gaa tac cga tct gtc gtt ttc caa	2210
Glu Met Ala Val Val Ala Thr Glu Glu Tyr Arg Ser Val Val Phe Gln	
720 725 730	
gaa cct cga ttc gtc gag tat ttc cgc ctc gct act ccg gag ctg gag	2258
Glu Pro Arg Phe Val Glu Tyr Phe Arg Leu Ala Thr Pro Glu Leu Glu	
735 740 745	
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Tyr Gly Arg Met Asn Ile Gly Ser Arg Pro Ser Lys Arg Lys Pro Ser	
750 755 760	
ggt ggg atc gaa tct ctc cgt gca atc cca tgg atc ttt gct tgg acg	2354
Gly Gly Ile Glu Ser Leu Arg Ala Ile Pro Trp Ile Phe Ala Trp Thr	
765 770 775	
caa aca aga ttc cat ctt cct gta tgg tta ggt ttc gga gca gca ttt	2402
Gln Thr Arg Phe His Leu Pro Val Trp Leu Gly Phe Gly Ala Ala Phe	
780 785 790 795	
agg tat gcg atc aag aag gat gtg aga aac ctt cac atg ctg caa gat	2450

Arg Tyr Ala Ile Lys Lys Asp Val Arg Asn Leu His Met Leu Gln Asp  
 800 805 810  
 atg tat aaa caa tgg ccc ttt ttc cga gtc acc atc gat cta att gaa 2498  
 Met Tyr Lys Gln Trp Pro Phe Phe Arg Val Thr Ile Asp Leu Ile Glu  
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 Met Val Phe Ala Lys Gly Asp Pro Gly Ile Ala Ala Leu Tyr Asp Lys  
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 gac ctt ctt gaa gga gat cct tac ttg aaa cag aga cta agg cta cgt 2690  
 Asp Leu Leu Glu Gly Asp Pro Tyr Leu Lys Gln Arg Leu Arg Leu Arg  
 880 885 890  
 gac tct tac att acg acc ctc aac gtt tgc caa gcc tac aca ttg aag 2738  
 Asp Ser Tyr Ile Thr Thr Leu Asn Val Cys Gln Ala Tyr Thr Leu Lys  
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 agg atc cgt gat gca aac tac aat gtg act ctg cga cca cac att tct 2786  
 Arg Ile Arg Asp Ala Asn Tyr Asn Val Thr Leu Arg Pro His Ile Ser  
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 aaa gag atc atg caa tca agc aaa tca gca caa gag ctc gtc aag ctt 2834  
 Lys Glu Ile Met Gln Ser Ser Lys Ser Ala Gln Glu Leu Val Lys Leu  
 925 930 935  
 aac ccc acg agt gaa tac gcg cct gga ctt gag gac aca ctt atc tta 2882  
 Asn Pro Thr Ser Glu Tyr Ala Pro Gly Leu Glu Asp Thr Leu Ile Leu  
 940 945 950 955  
 acc atg aag ggt att gct gca gga ttg caa aac acc ggt taa gtgagtca 2932  
 Thr Met Lys Gly Ile Ala Ala Gly Leu Gln Asn Thr Gly  
 960 965

&lt;210&gt; 14

&lt;211&gt; 968

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 14

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Arg Gln Leu Val Pro Ala Lys Val Ser Glu Asp Asp Lys Leu Val Glu  
 20 25 30

Tyr Asp Ala Leu Leu Leu Asp Arg Phe Leu Asp Ile Leu Gln Asp Leu



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His	Gly	Glu	Asp	Leu	Arg	Glu	Thr	Val	Gln	Glu	Leu	Tyr	Glu	Leu	Ser				
50						55					60								
Ala	Glu	Tyr	Glu	Gly	Lys	Arg	Glu	Pro	Ser	Lys	Leu	Glu	Glu	Leu	Gly				
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Ser	Val	Leu	Thr	Ser	Leu	Asp	Pro	Gly	Asp	Ser	Ile	Val	Ile	Ser	Lys				
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Ala	Phe	Ser	His	Met	Leu	Asn	Leu	Ala	Asn	Leu	Ala	Glu	Glu	Val	Gln				
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Ile	Ala	His	Arg	Arg	Arg	Ile	Lys	Lys	Leu	Lys	Lys	Gly	Asp	Phe	Val				
	115						120					125							
Asp	Glu	Ser	Ser	Ala	Thr	Thr	Glu	Ser	Asp	Ile	Glu	Glu	Thr	Phe	Lys				
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Arg	Leu	Val	Ser	Asp	Leu	Gly	Lys	Ser	Pro	Glu	Glu	Ile	Phe	Asp	Ala				
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Leu	Lys	Asn	Gln	Thr	Val	Asp	Leu	Val	Leu	Thr	Ala	His	Pro	Thr	Gln				
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Ser	Val	Arg	Arg	Ser	Leu	Leu	Gln	Lys	His	Gly	Arg	Ile	Arg	Asp	Cys				
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Leu	Ala	Gln	Leu	Tyr	Ala	Lys	Asp	Ile	Thr	Pro	Asp	Asp	Lys	Gln	Glu				
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Leu	Asp	Glu	Ser	Leu	Gln	Arg	Glu	Ile	Gln	Ala	Ala	Phe	Arg	Thr	Asp				
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Glu	Ile	Arg	Arg	Thr	Pro	Pro	Thr	Pro	Gln	Asp	Glu	Met	Arg	Ala	Gly				
225					230					235					240				
Met	Ser	Tyr	Phe	His	Glu	Thr	Ile	Trp	Lys	Gly	Val	Pro	Lys	Phe	Leu				
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Arg	Arg	Val	Asp	Thr	Ala	Leu	Lys	Asn	Ile	Gly	Ile	Asp	Glu	Arg	Val				
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Pro	Tyr	Asn	Ala	Pro	Leu	Ile	Gln	Phe	Ser	Ser	Trp	Met	Gly	Gly	Asp				
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Arg	Asp	Gly	Asn	Pro	Arg	Val	Thr	Pro	Glu	Val	Thr	Arg	Asp	Val	Cys				
290						295					300								
Leu	Leu	Ala	Arg	Met	Met	Ala	Ala	Asn	Leu	Tyr	Tyr	Asn	Gln	Ile	Glu				
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Asn	Leu	Met	Phe	Glu	Leu	Ser	Met	Trp	Arg	Cys	Thr	Asp	Glu	Phe	Arg				
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Val	Arg	Ala	Asp	Glu	Leu	His	Arg	Asn	Ser	Arg	Lys	Asp	Ala	Ala	Lys				

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His Tyr Ile Glu Phe Trp Lys Thr Ile Pro Pro Thr Glu Pro Tyr Arg	355		360		365
Val Ile Leu Gly Asp Val Arg Asp Lys Leu Tyr His Thr Arg Glu Arg	370		375		380
Ser Arg Gln Leu Leu Ser Asn Gly Ile Ser Asp Ile Pro Glu Glu Ala	385		390		395
Thr Phe Thr Asn Val Glu Gln Phe Leu Glu Pro Leu Glu Leu Cys Tyr		405		410	415
Arg Ser Leu Cys Ser Cys Gly Asp Ser Pro Ile Ala Asp Gly Ser Leu		420		425	430
Leu Asp Phe Leu Arg Gln Val Ser Thr Phe Gly Leu Ser Leu Val Arg		435		440	445
Leu Asp Ile Arg Gln Glu Ser Glu Arg His Thr Asp Val Leu Asp Ala		450		455	460
Ile Thr Lys His Leu Asp Ile Gly Ser Ser Tyr Arg Asp Trp Ser Glu		465		470	475
Glu Gly Arg Gln Glu Trp Leu Leu Ala Glu Leu Ser Gly Lys Arg Pro		485		490	495
Leu Phe Gly Pro Asp Leu Pro Lys Thr Glu Glu Ile Ser Asp Val Leu		500		505	510
Asp Thr Phe Lys Val Ile Ser Glu Leu Pro Ser Asp Cys Phe Gly Ala		515		520	525
Tyr Ile Ile Ser Met Ala Thr Ser Pro Ser Asp Val Leu Ala Val Glu		530		535	540
Leu Leu Gln Arg Glu Cys His Val Lys Asn Pro Leu Arg Val Val Pro		545		550	555
Leu Phe Glu Lys Leu Ala Asp Leu Glu Ala Ala Pro Ala Ala Val Ala		565		570	575
Arg Leu Phe Ser Ile Asp Trp Tyr Lys Asn Arg Ile Asn Gly Lys Gln		580		585	590
Glu Val Met Ile Gly Tyr Ser Asp Ser Gly Lys Asp Ala Gly Arg Leu		595		600	605
Ser Ala Ala Trp Glu Leu Tyr Lys Ala Gln Glu Glu Leu Val Lys Val		610		615	620
Ala Lys Lys Tyr Gly Val Lys Leu Thr Met Phe His Gly Arg Gly Gly		625		630	635
Thr Val Gly Arg Gly Gly Gly Pro Thr His Leu Ala Ile Leu Ser Gln					640

645										650					655				
Pro	Pro	Asp	Thr	Val	Asn	Gly	Ser	Leu	Arg	Val	Thr	Val	Gln	Gly	Glu				
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Val	Ile	Glu	Gln	Ser	Phe	Gly	Glu	Ala	His	Leu	Cys	Phe	Arg	Thr	Leu				
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Gln	Arg	Phe	Thr	Ala	Ala	Thr	Leu	Glu	His	Gly	Met	Asn	Pro	Pro	Ile				
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Ser	Pro	Lys	Pro	Glu	Trp	Arg	Ala	Leu	Leu	Asp	Glu	Met	Ala	Val	Val				
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Glu	Tyr	Phe	Arg	Leu	Ala	Thr	Pro	Glu	Leu	Glu	Tyr	Gly	Arg	Met	Asn				
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Ile	Gly	Ser	Arg	Pro	Ser	Lys	Arg	Lys	Pro	Ser	Gly	Gly	Ile	Glu	Ser				
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Leu	Arg	Ala	Ile	Pro	Trp	Ile	Phe	Ala	Trp	Thr	Gln	Thr	Arg	Phe	His				
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Leu	Pro	Val	Trp	Leu	Gly	Phe	Gly	Ala	Ala	Phe	Arg	Tyr	Ala	Ile	Lys				
785					790					795					800				
Lys	Asp	Val	Arg	Asn	Leu	His	Met	Leu	Gln	Asp	Met	Tyr	Lys	Gln	Trp				
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Pro	Phe	Phe	Arg	Val	Thr	Ile	Asp	Leu	Ile	Glu	Met	Val	Phe	Ala	Lys				
			820					825					830						
Gly	Asp	Pro	Gly	Ile	Ala	Ala	Leu	Tyr	Asp	Lys	Leu	Leu	Val	Ser	Glu				
		835					840					845							
Asp	Leu	Trp	Ala	Phe	Gly	Glu	Lys	Leu	Arg	Ala	Asn	Phe	Asp	Glu	Thr				
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Lys	Asn	Leu	Val	Leu	Gln	Thr	Ala	Gly	His	Lys	Asp	Leu	Leu	Glu	Gly				
865					870					875					880				
Asp	Pro	Tyr	Leu	Lys	Gln	Arg	Leu	Arg	Leu	Arg	Asp	Ser	Tyr	Ile	Thr				
			885					890						895					
Thr	Leu	Asn	Val	Cys	Gln	Ala	Tyr	Thr	Leu	Lys	Arg	Ile	Arg	Asp	Ala				
			900					905					910						
Asn	Tyr	Asn	Val	Thr	Leu	Arg	Pro	His	Ile	Ser	Lys	Glu	Ile	Met	Gln				
		915					920					925							
Ser	Ser	Lys	Ser	Ala	Gln	Glu	Leu	Val	Lys	Leu	Asn	Pro	Thr	Ser	Glu				
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945

950

955

960

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&lt;211&gt; 271

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (17)..(259)

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Gly Ser Ala Val Val Ala Tyr Val Cys Asp Lys Val Ile Ser Asp Asp  
15 20 25

aag ctt ttt gga ggt act aca cca gga act att act aac aag gaa tgg 148  
Lys Leu Phe Gly Gly Thr Thr Pro Gly Thr Ile Thr Asn Lys Glu Trp  
30 35 40

ggt gct gcg act gaa gag aga tta caa gca tgg cca aga gtt gct ggt 196  
Gly Ala Ala Thr Glu Glu Arg Leu Gln Ala Trp Pro Arg Val Ala Gly  
45 50 55 60

cct ccc gtc gtc atg aac cct atc agt cgc cag aat ttc atc gtc aag 244  
Pro Pro Val Val Met Asn Pro Ile Ser Arg Gln Asn Phe Ile Val Lys  
65 70 75

tca cgt cct gaa taa cttttgatgc ct 271  
Ser Arg Pro Glu  
80

&lt;210&gt; 16

&lt;211&gt; 80

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 16

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Val Ala Tyr Val Cys Asp Lys Val Ile Ser Asp Asp Lys Leu Phe Gly  
20 25 30

Gly Thr Thr Pro Gly Thr Ile Thr Asn Lys Glu Trp Gly Ala Ala Thr  
35 40 45

Glu Glu Arg Leu Gln Ala Trp Pro Arg Val Ala Gly Pro Pro Val Val  
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 Glu Tyr Leu Lys Glu Ile Thr Lys Ala Arg Arg Glu Leu Arg Ser Leu  
 10 15 20



atc gcg aac aag aac tgt gct cct atc atg ctc cga ttg gcg 143  
 Ile Ala Asn Lys Asn Cys Ala Pro Ile Met Leu Arg Leu Ala  
 25 30 35  
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 gtggagatcg ttcgattgta gttaggctgt agaatcgatt ttgtttgttt ttgaatgttg 263  
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 Trp His Asp Ala Gly Thr Tyr  
 40 45  
 gat gct caa tgc aag acc ggt gga cct aat ggc tct atc agg aac gaa 363  
 Asp Ala Gln Ser Lys Thr Gly Gly Pro Asn Gly Ser Ile Arg Asn Glu  
 50 55 60  
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 Glu Glu His Thr His Gly Ala Asn Ser Gly Leu Lys Ile Ala Leu Asp  
 65 70 75  
 ctc tgt ggtaggattt tgatttagtt tttgtagatt cactttctgg ataatttcat 467  
 Leu Cys  
 gcgatgtatc cgttttatgt tgtgggttaa gaacactggt caaaataatt acattatgct 527  
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 Glu  
 80  
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 Gly Val Lys Ala Lys His Pro Lys Ile Thr Tyr Ala Asp Leu Tyr Gln  
 85 90 95  
 gtgagttaag gctgtgagag aaatcttttt gatgtccttg ttgctttttc tgcacatttg 692  
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 aatttgtttc aggagatggt actgattgtg atttggttta caaaaatcat agattgacta 872  
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Ile Met Leu Arg Leu Ala Trp His Asp Ala Gly Thr Tyr Asp Ala Gln

35

40

45

Ser Lys Thr Gly Gly Pro Asn Gly Ser Ile Arg Asn Glu Glu Glu His

50

55

60

Thr His Gly Ala Asn Ser Gly Leu Lys Ile Ala Leu Asp Leu Cys Glu

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Gly Val Lys Ala Lys His Pro Lys Ile Thr Tyr Ala Asp Leu Tyr Gln

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Leu Ala Gly Val Val Ala Val Glu Val Thr Gly Gly Pro Asp Ile Val

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Phe Val Pro Gly Arg Lys Asp Ser Asn Val Cys Pro Lys Glu Gly Arg

115

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Ser	Ala	Thr	Tyr	Val	Gly	Val	Tyr	Asp	Gly	His	Gly	Gly	Pro	Glu	Ala	
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Ser	Arg	Ala	Val	Leu	Gly	Ser	Val	Val	Ser	Gly	Val	Asp	Ser	Asn	Lys	
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Gly	Ala	Val	Ala	Glu	Arg	Leu	Ser	Thr	Asp	His	Asn	Val	Ala	Val	Glu	
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Val	Leu	Tyr	Thr	Arg	Gly	Val	Trp	Arg	Ile	Lys	Gly	Ile	Ile	Gln		



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Ile Phe Ala Ser Asp Gly Leu Trp Glu His Leu Ser Asp Glu Thr Ala			
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 Lys Gly Ile Arg Arg His Phe His Asp Asp Ile Ser Val Ile Val Val  
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Lys Lys Asp Glu Ser Gly Leu Thr Ile Leu His Leu Asp Ser Leu Gly  
415 420 425

ctt cac tcg aga aaa tca att gtt gaa aat gta aaa ag gtgagatgct 2934  
Leu His Ser Arg Lys Ser Ile Val Glu Asn Val Lys Ar  
430 435

aggggcttta cccgtgactt tatgtttctca catgcttgac gttgtatgca tatggtttca 2994  
gttcataaaa ggaaaaatta ttacactggc ttgaaaatgt acgacattta ctagtttcta 3054  
tgtcaatttg ttgtag g ttt cta aaa gac gaa tgg aat tat ttg aat caa 3104  
g Phe Leu Lys Asp Glu Trp Asn Tyr Leu Asn Gln  
440 445 450

gat gac tat tcc ttg gat ctg cct atc tca gaa aaa gta tgg aaa aac 3152  
Asp Asp Tyr Ser Leu Asp Leu Pro Ile Ser Glu Lys Val Trp Lys Asn  
455 460 465

ctc cct cgt agg atc agc gaa gct gtt gtt cag gtcagtcttt taccttctta 3205  
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470 475

atcccatgat tcaaggaact ttgtttatac ggttttcttcg gaaatatgat tatattcaga 3265  
cactagaacc acaggaagtt caattcgtct tatgatatta ttctctttgt gcaaccag 3323  
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 Phe Asp Lys  
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Pro Pro Thr Phe Phe Ser Asp Asp Gln Thr Asp Ser Pro Lys Leu Leu  
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Thr Asp Arg Asp Leu Asp Glu Gln Leu Glu Arg Lys Lys Ala Ile Leu  
 65 70 75 80

Thr Leu Gly Pro Gly Leu Pro Asp Lys Gly Glu Lys Ile Arg Leu Lys  
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Ile Ala Asp Leu Glu Glu Glu Lys Gln Arg Ser Asp Val Leu Pro Gln  
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Gly Asn Ala Val Ser Lys Asp Thr Ser Arg Gly Asn Ala Asp Ser Lys  
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 Cys Ser Leu Gln Glu Asp Ile Cys Tyr Pro Thr ArSeg Phe Leu Gln  
                                  325                      330                      e                      335  
 Gln Gln Ile Ser Sr Ser Asn Gln Ile Ser Ala Asp Cys His Phe Phe  
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 Ser Gly Leu Thr Ile Leu His Leu Asp Ser Leu Gly Leu His Ser Arg  
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 Lys Ser Ile Val Glu Asn Val Lys Arg Phe Leu Lys Asp Glu Trp Asn  
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 Tyr Leu Asn Gln Asp Asp Tyr Ser Leu Asp Leu Pro Ile Ser Glu Lys

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 Gly Thr Arg Leu Arg Pro Leu Thr Leu Ser Phe Pro Lys Pro Leu Val  
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 Asp Phe Ala Asn Lys Pro Met Ile Leu His Gln Ile Glu Ala Leu Lys  
 30 35 40

gca gtt gga gtt gat gaa gtg gtt ttg gcc atc aat tat cag cca gag 195  
 Ala Val Gly Val Asp Glu Val Val Leu Ala Ile Asn Tyr Gln Pro Glu  
 45 50 55

gtg atg ctg aac ttc ttg aag gac ttt gag acc aag ctg gaa atc aaa 243  
 Val Met Leu Asn Phe Leu Lys Asp Phe Glu Thr Lys Leu Glu Ile Lys  
 60 65 70

atc act tgc tca caa gag acc gag cca cta ggt acc gct ggt cct ctg 291  
 Ile Thr Cys Ser Gln Glu Thr Glu Pro Leu Gly Thr Ala Gly Pro Leu  
 75 80 85 90

gct cta gcg aga gac aaa ttg ctt gat gga tct gga gag ccc ttc ttt 339  
 Ala Leu Ala Arg Asp Lys Leu Leu Asp Gly Ser Gly Glu Pro Phe Phe



95										100					105					
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Glu	Phe	His	Lys	Ser	His	Gly	Gly	Glu	Ala	Ser	Ile	Met	Val	Thr	Lys					
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Val	Asp	Glu	Pro	Ser	Lys	Tyr	Gly	Val	Val	Val	Met	Glu	Glu	Ser	Thr					
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Gly	Arg	Val	Glu	Lys	Phe	Val	Glu	Lys	Pro	Lys	Leu	Tyr	Val	Gly	Asn					
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Lys	Ile	Asn	Ala	Gly	Ile	Tyr	Leu	Leu	Asn	Pro	Ser	Val	Leu	Asp	Lys					
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Ile	Glu	Leu	Arg	Pro	Thr	Ser	Ile	Glu	Lys	Glu	Thr	Phe	Pro	Lys	Ile					
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Ala	Ala	Ala	Gln	Gly	Leu	Tyr	Ala	Met	Val	Leu	Pro	Gly	Phe	Trp	Met					
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Asp	Ser	Leu	Arg	Lys	Lys	Ser	Pro	Ala	Lys	Leu	Thr	Ser	Gly	Pro	His					
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Ile	Val	Gly	Asn	Val	Leu	Val	Asp	Glu	Thr	Ala	Thr	Ile	Gly	Glu	Gly					
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tgt	ttg	att	gga	cca	gac	gtt	gcc	att	ggg	cca	ggc	tgc	att	gtt	gag	867				
Cys	Leu	Ile	Gly	Pro	Asp	Val	Ala	Ile	Gly	Pro	Gly	Cys	Ile	Val	Glu					
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Ser	Gly	Val	Arg	Leu	Ser	Arg	Cys	Thr	Val	Met	Arg	Gly	Val	Arg	Ile					
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Leu	Leu	Asp	Gly	Ser	Gly	Glu	Pro	Phe	Phe	Val	Leu	Asn	Ser	Asp	Val		
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Ile	Ser	Glu	Tyr	Pro	Leu	Lys	Glu	Met	Leu	Glu	Phe	His	Lys	Ser	His		
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Gly	Gly	Glu	Ala	Ser	Ile	Met	Val	Thr	Lys	Val	Asp	Glu	Pro	Ser	Lys		
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Tyr	Leu	Leu	Asn	Pro	Ser	Val	Leu	Asp	Lys	Ile	Glu	Leu	Arg	Pro	Thr		
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Tyr Ala Met Val Leu Pro Gly Phe Trp Met Asp Ile Gly Gln Pro Arg  
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 Asp Tyr Ile Thr Gly Leu Arg Leu Tyr Leu Asp Ser Leu Arg Lys Lys  
 225 230 235 240  
 Ser Pro Ala Lys Leu Thr Ser Gly Pro His Ile Val Gly Asn Val Leu  
 245 250 255  
 Val Asp Glu Thr Ala Thr Ile Gly Glu Gly Cys Leu Ile Gly Pro Asp  
 260 265 270  
 Val Ala Ile Gly Pro Gly Cys Ile Val Glu Ser Gly Val Arg Leu Ser  
 275 280 285  
 Arg Cys Thr Val Met Arg Gly Val Arg Ile Lys Lys His Ala Cys Ile  
 290 295 300  
 Ser Ser Ser Ile Ile Gly Trp His Ser Thr Val Gly Gln Trp Ala Arg  
 305 310 315 320  
 Ile Glu Asn Met Thr Ile Leu Gly Glu Asp Val His Val Ser Asp Glu  
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 Pro Tyr Arg Thr Asn Ser Ser Phe Gly Ser Lys Ser Ser Leu Leu Phe  
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cgg tct cca tcc tcc tcc tcc tca gtc tct atg acg aca acg cgt gga 146  
 Arg Ser Pro Ser Ser Ser Ser Ser Val Ser Met Thr Thr Thr Arg Gly  
 35 40 45

aac gtg gct gtg gcg gct gct gct aca tcc act gag gcg cta aga aaa 194  
 Asn Val Ala Val Ala Ala Ala Ala Thr Ser Thr Glu Ala Leu Arg Lys  
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gga ata gcg gag ttc tac aat gaa act tcg ggt ttg tgg gaa gag att	242
Gly Ile Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile	
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Trp Gly Asp His Met His His Gly Phe Tyr Asp Pro Asp Ser Ser Val	
80 85 90	
caa ctt tct gat tct ggt cac aag gaa gct cag atc cgt atg att gaa	338
Gln Leu Ser Asp Ser Gly His Lys Glu Ala Gln Ile Arg Met Ile Glu	
95 100 105 110	
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Glu Ser Leu Arg Phe Ala Gly Val Thr Asp Glu Glu Glu Glu Lys Lys	
115 120 125	
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Ile Lys Lys Val Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg	
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Tyr Leu Ala Ser Lys Phe Gly Ala Glu Cys Ile Gly Ile Thr Leu Ser	
145 150 155	
cct gtt cag gcc aag aga gcc aat gat ctc gcg gct gct caa tca ctc	530
Pro Val Gln Ala Lys Arg Ala Asn Asp Leu Ala Ala Ala Gln Ser Leu	
160 165 170	
tct cat aag gct tcc ttc caa gtt gcg gat gcg ttg gat cag cca ttc	578
Ser His Lys Ala Ser Phe Gln Val Ala Asp Ala Leu Asp Gln Pro Phe	
175 180 185 190	
gaa gat gga aaa ttc gat cta gtg tgg tcg atg gag agt ggt gag cat	626
Glu Asp Gly Lys Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His	
195 200 205	
atg cct gac aag gcc aag ttt gta aaa gag ttg gta cgt gtg gcg gct	674
Met Pro Asp Lys Ala Lys Phe Val Lys Glu Leu Val Arg Val Ala Ala	
210 215 220	
cca gga ggt agg ata ata ata gtg aca tgg tgc cat aga aat cta tct	722
Pro Gly Gly Arg Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Ser	
225 230 235	
gcg ggg gag gaa gct ttg cag ccg tgg gag caa aac atc ttg gac aaa	770
Ala Gly Glu Glu Ala Leu Gln Pro Trp Glu Gln Asn Ile Leu Asp Lys	
240 245 250	
atc tgt aag acg ttc tat ctc ccg gct tgg tgc tcc acc gat gat tat	818
Ile Cys Lys Thr Phe Tyr Leu Pro Ala Trp Cys Ser Thr Asp Asp Tyr	
255 260 265 270	
gtc aac ttg ctt caa tcc cat tct ctc cag gat att aag tgt gcg gat	866
Val Asn Leu Leu Gln Ser His Ser Leu Gln Asp Ile Lys Cys Ala Asp	
275 280 285	

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 Trp Ser Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Arg Thr Ala  
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                   305                  310                  315

att aaa gga gca ttg aca atg cca ttg atg att gaa ggt tac aag aaa 1010  
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ggt gtc att aag ttt ggt atc atc act tgc cag aag cca ctc taa 1055  
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Pro Ser Ser Ser Ser Ser Val Ser Met Thr Thr Thr Arg Gly Asn Val  
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Ala Val Ala Ala Ala Ala Thr Ser Thr Glu Ala Leu Arg Lys Gly Ile  
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Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile Trp Gly  
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Ser Asp Ser Gly His Lys Glu Ala Gln Ile Arg Met Ile Glu Glu Ser  
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Leu Arg Phe Ala Gly Val Thr Asp Glu Glu Glu Glu Lys Lys Ile Lys  
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Gln Ala Lys Arg Ala Asn Asp Leu Ala Ala Ala Gln Ser Leu Ser His  
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 195 200 205  
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 210 215 220  
 Gly Arg Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Ser Ala Gly  
 225 230 235 240  
 Glu Glu Ala Leu Gln Pro Trp Glu Gln Asn Ile Leu Asp Lys Ile Cys  
 245 250 255  
 Lys Thr Phe Tyr Leu Pro Ala Trp Cys Ser Thr Asp Asp Tyr Val Asn  
 260 265 270  
 Leu Leu Gln Ser His Ser Leu Gln Asp Ile Lys Cys Ala Asp Trp Ser  
 275 280 285  
 Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Arg Thr Ala Leu Thr  
 290 295 300  
 Trp Lys Gly Leu Val Ser Leu Leu Arg Ser Gly Met Lys Ser Ile Lys  
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 Leu Glu Ile Asp Asp Asp Gln Lys Leu Arg Ala Phe Tyr Asp Lys Arg  
 20 25 30  
 atc tct caa gaa gtc agt gga gat gct ttg ggc gag gag ttc aaa gga 143  
 Ile Ser Gln Glu Val Ser Gly Asp Ala Leu Gly Glu Glu Phe Lys Gly  
 35 40 45

tac gtt ttc aag atc aag ggt ggt tgc gat aag caa ggt ttc cca atg	191
Tyr Val Phe Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met	
50 55 60	
aag cag gga gtt ttg act cca ggc cgt gtt cgc ctt ttg ctt cac cga	239
Lys Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg	
65 70 75	
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Gly Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg Arg	
80 85 90 95	
aga aag tct gtt cgt ggt tgc att gtg agc cct gat ctc tct gtt ctg	335
Arg Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu	
100 105 110	
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Asn Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr	
115 120 125	
gat cat gag agc aag atg aga gga cca aag aga gcc tcc aag atc cgt	431
Asp His Glu Ser Lys Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg	
130 135 140	
aaa ctg ttt aac ctc aag aag gaa gat gat gtc agg acc tat gtc aac	479
Lys Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn	
145 150 155	
act tac cgc cgc aag ttc aca aac aag aag ggc aag gaa gtt agc aaa	527
Thr Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys	
160 165 170 175	
gcc cct aag atc cag agg ctt gtg acc cca ttg act ctt cag agg aag	575
Ala Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys	
180 185 190	
aga gct aga att gct gac aag aag aag aaa att gct aag gct aat tct	623
Arg Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser	
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Gln	Ile	Pro	Gln	Tyr	Phe	Ile	Leu	Gly	Ala	Ala	Glu	Val	Phe	Tyr	Phe	
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Lys	Val	Val	Glu	Leu	Ala	Thr	Val	Asn	Gly	Ala	Lys	Ser	Met	Lys	Gly	
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Thr	Pro	Tyr	Trp	Met	Ala	Pro	Glu	Val	Ile	Leu	Gln	Thr	Gly	His	Ser	
			240					245					250			
ttc	tct	gct	gat	ata	tgg	agt	ggt	ggg	tgc	act	gtg	att	gag	atg	gct	820
Phe	Ser	Ala	Asp	Ile	Trp	Ser	Val	Gly	Cys	Thr	Val	Ile	Glu	Met	Ala	
			255					260					265			
acg	ggg	aag	cct	ccc	tgg	agc	gag	cag	tat	cag	cag	ttt	gct	gct	gtc	868
Thr	Gly	Lys	Pro	Pro	Trp	Ser	Glu	Gln	Tyr	Gln	Gln	Phe	Ala	Ala	Val	
		270					275					280				
ctt	cat	att	ggg	aga	aca	aaa	gct	cat	cct	cca	att	cca	gaa	gac	ctc	916
Leu	His	Ile	Gly	Arg	Thr	Lys	Ala	His	Pro	Pro	Ile	Pro	Glu	Asp	Leu	
	285					290					295					
tca	cca	gag	gct	aaa	gac	ttt	cta	atg	aaa	tgc	tta	cac	aaa	gaa	cca	964
Ser	Pro	Glu	Ala	Lys	Asp	Phe	Leu	Met	Lys	Cys	Leu	His	Lys	Glu	Pro	

300	305	310	315	
agc ttg aga ctc tct gca acc gaa ttg ctt cag cac ccg ttt gtc act Ser Leu Arg Leu Ser Ala Thr Glu Leu Leu Gln His Pro Phe Val Thr	320	325	330	1012
gga aag cgc cag gaa cct tat cca gct tac cgt aat tct ctt acg gaa Gly Lys Arg Gln Glu Pro Tyr Pro Ala Tyr Arg Asn Ser Leu Thr Glu	335	340	345	1060
tgt gga aac cca ata act act caa gga atg aat gtt cgg agt tca ata Cys Gly Asn Pro Ile Thr Thr Gln Gly Met Asn Val Arg Ser Ser Ile	350	355	360	1108
aat tcg ttg atc agg agg tcg aca tgt tca ggc ttg aag gat gtc tgt Asn Ser Leu Ile Arg Arg Ser Thr Cys Ser Gly Leu Lys Asp Val Cys	365	370	375	1156
gaa ctg gga agc ttg agg agt tcc att ata tac cca cag aag tca aat Glu Leu Gly Ser Leu Arg Ser Ser Ile Ile Tyr Pro Gln Lys Ser Asn	380	385	390	1204
aac tca gga ttt ggt tgg cga gat gga gac tct gat gac ctt tgt cag Asn Ser Gly Phe Gly Trp Arg Asp Gly Asp Ser Asp Asp Leu Cys Gln	400	405	410	1252
acc gat atg gat gat ctc tgc aac att gaa tca gtc aga aac aat gtt Thr Asp Met Asp Asp Leu Cys Asn Ile Glu Ser Val Arg Asn Asn Val	415	420	425	1300
ttg tca cag tcc acc gat tta aac aag agt ttt aat ccc atg tgt gat Leu Ser Gln Ser Thr Asp Leu Asn Lys Ser Phe Asn Pro Met Cys Asp	430	435	440	1348
tcc acg gat aac tgg tct tgc aag ttt gat gaa agc cca aaa gtg atg Ser Thr Asp Asn Trp Ser Cys Lys Phe Asp Glu Ser Pro Lys Val Met	445	450	455	1396
aaa agc aaa tct aac ctg ctt tct tac caa gct tct caa ctc caa act Lys Ser Lys Ser Asn Leu Leu Ser Tyr Gln Ala Ser Gln Leu Gln Thr	460	465	470	1444
gga gtt cca tgt gat gag gaa acc agc tta aca ttt gct ggt ggc tct Gly Val Pro Cys Asp Glu Glu Thr Ser Leu Thr Phe Ala Gly Gly Ser	480	485	490	1492
tcc gtt gca gag gat gat tat aaa ggc aca gag ttg aaa ata aaa tca Ser Val Ala Glu Asp Asp Tyr Lys Gly Thr Glu Leu Lys Ile Lys Ser	495	500	505	1540
ttt ttg gat gag aag gct cag gat ttg aaa agg ttg cag acc cct ctg Phe Leu Asp Glu Lys Ala Gln Asp Leu Lys Arg Leu Gln Thr Pro Leu	510	515	520	1588
ctt gaa gaa ttc cac aat gct atg aat cca gga ata ccc caa ggt gca Leu Glu Glu Phe His Asn Ala Met Asn Pro Gly Ile Pro Gln Gly Ala	525	530	535	1636

ctt gga gac acc aat atc tac aat tta cca aac tta cca agt ata agc 1684  
 Leu Gly Asp Thr Asn Ile Tyr Asn Leu Pro Asn Leu Pro Ser Ile Ser  
 540 545 550 555  
 aag aca cct aaa cga ctt ccg agt aga cga ctc tca gca atc agt gat 1732  
 Lys Thr Pro Lys Arg Leu Pro Ser Arg Arg Leu Ser Ala Ile Ser Asp  
 560 565 570  
 gct atg ccc agc cca ctc aaa agc tcc aaa cgt aca ctg aac aca agc 1780  
 Ala Met Pro Ser Pro Leu Lys Ser Ser Lys Arg Thr Leu Asn Thr Ser  
 575 580 585  
 aga gtg atg cag tca gga act gaa cca act caa gtc aac gag tcg acc 1828  
 Arg Val Met Gln Ser Gly Thr Glu Pro Thr Gln Val Asn Glu Ser Thr  
 590 595 600  
 aag aag gga gta aat aat agc cgt tgt ttc tca gag ata cgt cgg aag 1876  
 Lys Lys Gly Val Asn Asn Ser Arg Cys Phe Ser Glu Ile Arg Arg Lys  
 605 610 615  
 tgg gaa gaa gaa ctc tat gaa gag ctt gag agg cat cga gag aat ctg 1924  
 Trp Glu Glu Glu Leu Tyr Glu Glu Leu Glu Arg His Arg Glu Asn Leu  
 620 625 630 635  
 cga cac gct ggt gca gga ggg aag act cca tta tca ggc cac aaa gga 1972  
 Arg His Ala Gly Ala Gly Gly Lys Thr Pro Leu Ser Gly His Lys Gly  
 640 645 650  
 tag tgaacggct 1984

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 <212> PRT  
 <213> Arabidopsis thaliana

<400> 34

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 20 25 30  
 Val Gly Lys Ile Asn Ser Ser Ile Arg Ser Ser Arg Ile Gly Leu Phe  
 35 40 45  
 Ser Lys Pro Pro Pro Gly Leu Pro Ala Pro Arg Lys Glu Glu Ala Pro  
 50 55 60  
 Ser Ile Arg Trp Arg Lys Gly Glu Leu Ile Gly Cys Gly Ala Phe Gly  
 65 70 75 80  
 Arg Val Tyr Met Gly Met Asn Leu Asp Ser Gly Glu Leu Leu Ala Ile  
 85 90 95

Lys Gln Val Leu Ile Ala Pro Ser Ser Ala Ser Lys Glu Lys Thr Gln  
 100 105 110  
 Gly His Ile Arg Glu Leu Glu Glu Glu Val Gln Leu Leu Lys Asn Leu  
 115 120 125  
 Ser His Pro Asn Ile Val Arg Tyr Leu Gly Thr Val Arg Glu Ser Asp  
 130 135 140  
 Ser Leu Asn Ile Leu Met Glu Phe Val Pro Gly Gly Ser Ile Ser Ser  
 145 150 155 160  
 Leu Leu Glu Lys Phe Gly Ser Phe Pro Glu Pro Val Ile Ile Met Tyr  
 165 170 175  
 Thr Lys Gln Leu Leu Leu Gly Leu Glu Tyr Leu His Asn Asn Gly Ile  
 180 185 190  
 Met His Arg Asp Ile Lys Gly Ala Asn Ile Leu Val Asp Asn Lys Gly  
 195 200 205  
 Cys Ile Arg Leu Ala Asp Phe Gly Ala Ser Lys Lys Val Val Glu Leu  
 210 215 220  
 Ala Thr Val Asn Gly Ala Lys Ser Met Lys Gly Thr Pro Tyr Trp Met  
 225 230 235 240  
 Ala Pro Glu Val Ile Leu Gln Thr Gly His Ser Phe Ser Ala Asp Ile  
 245 250 255  
 Trp Ser Val Gly Cys Thr Val Ile Glu Met Ala Thr Gly Lys Pro Pro  
 260 265 270  
 Trp Ser Glu Gln Tyr Gln Gln Phe Ala Ala Val Leu His Ile Gly Arg  
 275 280 285  
 Thr Lys Ala His Pro Pro Ile Pro Glu Asp Leu Ser Pro Glu Ala Lys  
 290 295 300  
 Asp Phe Leu Met Lys Cys Leu His Lys Glu Pro Ser Leu Arg Leu Ser  
 305 310 315 320  
 Ala Thr Glu Leu Leu Gln His Pro Phe Val Thr Gly Lys Arg Gln Glu  
 325 330 335  
 Pro Tyr Pro Ala Tyr Arg Asn Ser Leu Thr Glu Cys Gly Asn Pro Ile  
 340 345 350  
 Thr Thr Gln Gly Met Asn Val Arg Ser Ser Ile Asn Ser Leu Ile Arg  
 355 360 365  
 Arg Ser Thr Cys Ser Gly Leu Lys Asp Val Cys Glu Leu Gly Ser Leu  
 370 375 380  
 Arg Ser Ser Ile Ile Tyr Pro Gln Lys Ser Asn Asn Ser Gly Phe Gly  
 385 390 395 400

Trp Arg Asp Gly Asp Ser Asp Asp Leu Cys Gln Thr Asp Met Asp Asp  
 405 410 415  
 Leu Cys Asn Ile Glu Ser Val Arg Asn Asn Val Leu Ser Gln Ser Thr  
 420 425 430  
 Asp Leu Asn Lys Ser Phe Asn Pro Met Cys Asp Ser Thr Asp Asn Trp  
 435 440 445  
 Ser Cys Lys Phe Asp Glu Ser Pro Lys Val Met Lys Ser Lys Ser Asn  
 450 455 460  
 Leu Leu Ser Tyr Gln Ala Ser Gln Leu Gln Thr Gly Val Pro Cys Asp  
 465 470 475 480  
 Glu Glu Thr Ser Leu Thr Phe Ala Gly Gly Ser Ser Val Ala Glu Asp  
 485 490 495  
 Asp Tyr Lys Gly Thr Glu Leu Lys Ile Lys Ser Phe Leu Asp Glu Lys  
 500 505 510  
 Ala Gln Asp Leu Lys Arg Leu Gln Thr Pro Leu Leu Glu Glu Phe His  
 515 520 525  
 Asn Ala Met Asn Pro Gly Ile Pro Gln Gly Ala Leu Gly Asp Thr Asn  
 530 535 540  
 Ile Tyr Asn Leu Pro Asn Leu Pro Ser Ile Ser Lys Thr Pro Lys Arg  
 545 550 555 560  
 Leu Pro Ser Arg Arg Leu Ser Ala Ile Ser Asp Ala Met Pro Ser Pro  
 565 570 575  
 Leu Lys Ser Ser Lys Arg Thr Leu Asn Thr Ser Arg Val Met Gln Ser  
 580 585 590  
 Gly Thr Glu Pro Thr Gln Val Asn Glu Ser Thr Lys Lys Gly Val Asn  
 595 600 605  
 Asn Ser Arg Cys Phe Ser Glu Ile Arg Arg Lys Trp Glu Glu Glu Leu  
 610 615 620  
 Tyr Glu Glu Leu Glu Arg His Arg Glu Asn Leu Arg His Ala Gly Ala  
 625 630 635 640  
 Gly Gly Lys Thr Pro Leu Ser Gly His Lys Gly  
 645 650

&lt;210&gt; 35

&lt;211&gt; 1736

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1605)

&lt;400&gt; 35

atg ccc cct cct aag atg ctt cca cca acg gca agg gat tca gta gca	48
Met Pro Pro Pro Lys Met Leu Pro Pro Thr Ala Arg Asp Ser Val Ala	
1 5 10 15	
ggg aca ggg ggt agt cca cca cct cca cct cca cca cca gct cgg tgg	96
Gly Thr Gly Gly Ser Pro Pro Pro Pro Pro Pro Pro Pro Ala Arg Trp	
20 25 30	
agg gta gcg ggg gag gga gga ttg gat aca aca cca ccg ccg ccc cct	144
Arg Val Ala Gly Glu Gly Gly Leu Asp Thr Thr Pro Pro Pro Pro	
35 40 45	
cca acg gca gat aca gtc gtg gcg gga agg acg agt tta ggt gag gcg	192
Pro Thr Ala Asp Thr Val Val Ala Gly Arg Thr Ser Leu Gly Glu Ala	
50 55 60	
ccc cct cct cgt cag cct cca cgt cct cca aca gca cgg tgg tca gcg	240
Pro Pro Pro Arg Gln Pro Pro Arg Pro Pro Thr Ala Arg Trp Ser Ala	
65 70 75 80	
atg ggc aga gtg atg tgc agt ccg ccg ata cca cta tcg cgg agt aga	288
Met Gly Arg Val Met Cys Ser Pro Pro Ile Pro Leu Ser Arg Ser Arg	
85 90 95	
cta gcg ctt gac gac caa cgt tgg ccg gat tgg aca acg aac ggt tgg	336
Leu Ala Leu Asp Asp Gln Arg Trp Pro Asp Trp Thr Thr Asn Gly Trp	
100 105 110	
cta agc atg aga ccg acg tcc tcg cca aca agg cga att gac cca caa	384
Leu Ser Met Arg Pro Thr Ser Ser Pro Thr Arg Arg Ile Asp Pro Gln	
115 120 125	
ggg gcc cga cga tcc tca gtg tca cca gcg ccg gtg aca acg ggg atg	432
Gly Ala Arg Arg Ser Ser Val Ser Pro Ala Pro Val Thr Thr Gly Met	
130 135 140	
gcc acc tct cgc act gac gat acg cta ata gag gca gag acc ggt cgc	480
Ala Thr Ser Arg Thr Asp Asp Thr Leu Ile Glu Ala Glu Thr Gly Arg	
145 150 155 160	
gac tgg acg agg aaa cga atg gtc agg aaa ttg ctt aaa gca agg gcg	528
Asp Trp Thr Arg Lys Arg Met Val Arg Lys Leu Leu Lys Ala Arg Ala	
165 170 175	
aaa gac tac aag gag ggg gga att gcg gca tac ttt ggt tta cga gtg	576
Lys Asp Tyr Lys Glu Gly Gly Ile Ala Ala Tyr Phe Gly Leu Arg Val	
180 185 190	
ctg cga tgc tac tcg agg atc gta cga tcg atg aaa cgc cca ggc aac	624
Leu Arg Cys Tyr Ser Arg Ile Val Arg Ser Met Lys Arg Pro Gly Asn	
195 200 205	
ttg aaa ttc acg tgc cgg agg gat gtg gca ata gcc acg ttc agc ggc	672
Leu Lys Phe Thr Cys Arg Arg Asp Val Ala Ile Ala Thr Phe Ser Gly	



210	215	220	
aca ggc aga atg cag ctg agt atg aac agc cgt ttg cga gtc gag agc			720
Thr Gly Arg Met Gln Leu Ser Met Asn Ser Arg Leu Arg Val Glu Ser			
225	230	235	240
ctc gtg tcc gcg ggc cag agc gtg gcg tca ttc tgc ctt ttc ctg ata			768
Leu Val Ser Ala Gly Gln Ser Val Ala Ser Phe Cys Leu Phe Leu Ile			
	245	250	255
tgc acg gcg ccc tcg gcg atg cgg ctg gtt agc ctt ctt aca ctg acc			816
Cys Thr Ala Pro Ser Ala Met Arg Leu Val Ser Leu Leu Thr Leu Thr			
	260	265	270
cca agc atg acc tac cta aca tgc ggg ctg gga tgg atg acc gtc gtc			864
Pro Ser Met Thr Tyr Leu Thr Cys Gly Leu Gly Trp Met Thr Val Val			
	275	280	285
gta ctg ccg gcg ata gtg gtc cac tgt tat atg cgc cga cat acg gaa			912
Val Leu Pro Ala Ile Val Val His Cys Tyr Met Arg Arg His Thr Glu			
	290	295	300
ggg gga tgg cgg tat gcg gca ctc gag gag cat aag acg gag ccg gga			960
Gly Gly Trp Arg Tyr Ala Ala Leu Glu Glu His Lys Thr Glu Pro Gly			
	305	310	320
cga aat gaa aag atc acc cgg agt aga cgc aac tcg gcg ttc ggc ggg			1008
Arg Asn Glu Lys Ile Thr Arg Ser Arg Arg Asn Ser Ala Phe Gly Gly			
	325	330	335
ctg gtc ggt cga aat aaa aga cga aag aag tcc aag gtc tcc ggg gca			1056
Leu Val Gly Arg Asn Lys Arg Arg Lys Lys Ser Lys Val Ser Gly Ala			
	340	345	350
ccg aca gcg gtt tac aca gcg atg ttt ttc atg ttc tcc acg gca atc			1104
Pro Thr Ala Val Tyr Thr Ala Met Phe Phe Met Phe Ser Thr Ala Ile			
	355	360	365
aag ggg atg gtg gtg tgc aca atg aaa aaa aaa gtc aaa aaa agt gcg			1152
Lys Gly Met Val Val Cys Thr Met Lys Lys Lys Val Lys Lys Ser Ala			
	370	375	380
aat cgc aga ctc cgc cag ttg ctc cga tgg gcg cga tac cac gcg aac			1200
Asn Arg Arg Leu Arg Gln Leu Leu Arg Trp Ala Arg Tyr His Ala Asn			
	385	390	400
gcg ttc ttg ctc tgt tct ctt gca tgc gca cga ttc gcg gca tcg cga			1248
Ala Phe Leu Leu Cys Ser Leu Ala Cys Ala Arg Phe Ala Ala Ser Arg			
	405	410	415
acg gtc atc cat tgc agt att tac cca cgt ttc ggc ccc tta gcc acg			1296
Thr Val Ile His Cys Ser Ile Tyr Pro Arg Phe Gly Pro Leu Ala Thr			
	420	425	430
gtg acg gcc ata tgt ttg ata cta cac acg tgt acg tac cga cgt acg			1344
Val Thr Ala Ile Cys Leu Ile Leu His Thr Cys Thr Tyr Arg Arg Thr			
	435	440	445

gag gca gac acg acg cga cac gaa aat gac gac gcc cgg aag gtg atg 1392  
 Glu Ala Asp Thr Thr Arg His Glu Asn Asp Asp Ala Arg Lys Val Met  
 450 455 460  
 gaa gac atg gcc aaa cga atg gac gat agt agc agt ggg agc acg ttg 1440  
 Glu Asp Met Ala Lys Arg Met Asp Asp Ser Ser Ser Gly Ser Thr Leu  
 465 470 475 480  
 agc acg ctc acg act gac gag acg tac cac acc acc acg gag gtg acc 1488  
 Ser Thr Leu Thr Thr Asp Glu Thr Tyr His Thr Thr Thr Glu Val Thr  
 485 490 495  
 gat ttt gat tca tct cca tcg tgg gga cga tgc tca tcg cgg cgc ccg 1536  
 Asp Phe Asp Ser Ser Pro Ser Trp Gly Arg Cys Ser Ser Arg Arg Pro  
 500 505 510  
 ccg gcg ctg ctg gaa tcg aca ttt cgg cga tcc ccg aga ggg tcg acg 1584  
 Pro Ala Leu Leu Glu Ser Thr Phe Arg Arg Ser Pro Arg Gly Ser Thr  
 515 520 525  
 gga cga cga tgg cga gag tag attcggagtc aggaacgttg gaccgacagg 1635  
 Gly Arg Arg Trp Arg Glu  
 530 535  
 tggaccggtt tagggcagtt gacggtaggg gttgcctgac cagccttgac gctcgacagc 1695  
 taaaaaaaaac caacaaaaaaaa aaaaaaaaaaac aaaaaaaaaa a 1736

<210> 36  
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 <212> PRT  
 <213> Arabidopsis thaliana

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 Gly Thr Gly Gly Ser Pro Pro Pro Pro Pro Pro Pro Ala Arg Trp  
 20 25 30  
 Arg Val Ala Gly Glu Gly Gly Leu Asp Thr Thr Pro Pro Pro Pro Pro  
 35 40 45  
 Pro Thr Ala Asp Thr Val Val Ala Gly Arg Thr Ser Leu Gly Glu Ala  
 50 55 60  
 Pro Pro Pro Arg Gln Pro Pro Arg Pro Pro Thr Ala Arg Trp Ser Ala  
 65 70 75 80  
 Met Gly Arg Val Met Cys Ser Pro Pro Ile Pro Leu Ser Arg Ser Arg  
 85 90 95  
 Leu Ala Leu Asp Asp Gln Arg Trp Pro Asp Trp Thr Thr Asn Gly Trp  
 100 105 110

Leu Ser Met Arg Pro Thr Ser Ser Pro Thr Arg Arg Ile Asp Pro Gln  
 115 120 125  
 Gly Ala Arg Arg Ser Ser Val Ser Pro Ala Pro Val Thr Thr Gly Met  
 130 135 140  
 Ala Thr Ser Arg Thr Asp Asp Thr Leu Ile Glu Ala Glu Thr Gly Arg  
 145 150 155 160  
 Asp Trp Thr Arg Lys Arg Met Val Arg Lys Leu Leu Lys Ala Arg Ala  
 165 170 175  
 Lys Asp Tyr Lys Glu Gly Gly Ile Ala Ala Tyr Phe Gly Leu Arg Val  
 180 185 190  
 Leu Arg Cys Tyr Ser Arg Ile Val Arg Ser Met Lys Arg Pro Gly Asn  
 195 200 205  
 Leu Lys Phe Thr Cys Arg Arg Asp Val Ala Ile Ala Thr Phe Ser Gly  
 210 215 220  
 Thr Gly Arg Met Gln Leu Ser Met Asn Ser Arg Leu Arg Val Glu Ser  
 225 230 235 240  
 Leu Val Ser Ala Gly Gln Ser Val Ala Ser Phe Cys Leu Phe Leu Ile  
 245 250 255  
 Cys Thr Ala Pro Ser Ala Met Arg Leu Val Ser Leu Leu Thr Leu Thr  
 260 265 270  
 Pro Ser Met Thr Tyr Leu Thr Cys Gly Leu Gly Trp Met Thr Val Val  
 275 280 285  
 Val Leu Pro Ala Ile Val Val His Cys Tyr Met Arg Arg His Thr Glu  
 290 295 300  
 Gly Gly Trp Arg Tyr Ala Ala Leu Glu Glu His Lys Thr Glu Pro Gly  
 305 310 315 320  
 Arg Asn Glu Lys Ile Thr Arg Ser Arg Arg Asn Ser Ala Phe Gly Gly  
 325 330 335  
 Leu Val Gly Arg Asn Lys Arg Arg Lys Lys Ser Lys Val Ser Gly Ala  
 340 345 350  
 Pro Thr Ala Val Tyr Thr Ala Met Phe Phe Met Phe Ser Thr Ala Ile  
 355 360 365  
 Lys Gly Met Val Val Cys Thr Met Lys Lys Lys Val Lys Lys Ser Ala  
 370 375 380  
 Asn Arg Arg Leu Arg Gln Leu Leu Arg Trp Ala Arg Tyr His Ala Asn  
 385 390 395 400  
 Ala Phe Leu Leu Cys Ser Leu Ala Cys Ala Arg Phe Ala Ala Ser Arg  
 405 410 415

Thr Val Ile His Cys Ser Ile Tyr Pro Arg Phe Gly Pro Leu Ala Thr  
 420 425 430  
 Val Thr Ala Ile Cys Leu Ile Leu His Thr Cys Thr Tyr Arg Arg Thr  
 435 440 445  
 Glu Ala Asp Thr Thr Arg His Glu Asn Asp Asp Ala Arg Lys Val Met  
 450 455 460  
 Glu Asp Met Ala Lys Arg Met Asp Asp Ser Ser Ser Gly Ser Thr Leu  
 465 470 475 480  
 Ser Thr Leu Thr Thr Asp Glu Thr Tyr His Thr Thr Thr Glu Val Thr  
 485 490 495  
 Asp Phe Asp Ser Ser Pro Ser Trp Gly Arg Cys Ser Ser Arg Arg Pro  
 500 505 510  
 Pro Ala Leu Leu Glu Ser Thr Phe Arg Arg Ser Pro Arg Gly Ser Thr  
 515 520 525  
 Gly Arg Arg Trp Arg Glu  
 530

<210> 37  
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 <212> DNA  
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<220>  
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 1 5 10

gct aag aag ggt gcc aac ctc ttc aag gtacgaacag agcaaagatg 97  
 Ala Lys Lys Gly Ala Asn Leu Phe Lys  
 15 20

ccgctgaaaa ttctcacggc gcattctatc ccgcagaact tttctgacca ctttgtag 155

acc cgc tgc gct cag tgc cac acc ctg aag gcc ggc gag ggc aac aag 203  
 Thr Arg Cys Ala Gln Cys His Thr Leu Lys Ala Gly Glu Gly Asn Lys  
 25 30 35

att ggc cct gag ctc cac ggt ctc ttc ggc cgc aag act ggt tcc gtc 251  
 Ile Gly Pro Glu Leu His Gly Leu Phe Gly Arg Lys Thr Gly Ser Val  
                     40                    45                    50

gct ggc tac tca tac acc gac gcc aac aag cag aag ggt atc gag tgg 299  
 Ala Gly Tyr Ser Tyr Thr Asp Ala Asn Lys Gln Lys Gly Ile Glu Trp  
                     55                    60                    65

aag gac gac act ctc gtacgtcacg ccaccggaag attgaaatgt ccccgagacc 354  
 Lys Asp Asp Thr Leu  
                     70

ctccgctaac acgacacag ttc gag tac ctc gag aac ccc aag aag tac att 406  
                                     Phe Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile  
                                     75                                    80

ccc ggt acc aag atg gcc ttc ggt ggt ctc aag aag ccc aag gac cgc 454  
 Pro Gly Thr Lys Met Ala Phe Gly Gly Leu Lys Lys Pro Lys Asp Arg  
                     85                    90                    95                    100

aac gac ctc atc acc ttc ctt gag gag gag acc aaa taa gcgtcttgct 503  
 Asn Asp Leu Ile Thr Phe Leu Glu Glu Glu Thr Lys  
                     105                    110

acccc 508

<210> 38  
 <211> 112  
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 <213> Arabidopsis thaliana

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Asn Leu Phe Lys Thr Arg Cys Ala Gln Cys His Thr Leu Lys Ala Gly  
                     20                    25                    30

Glu Gly Asn Lys Ile Gly Pro Glu Leu His Gly Leu Phe Gly Arg Lys  
                     35                    40                    45

Thr Gly Ser Val Ala Gly Tyr Ser Tyr Thr Asp Ala Asn Lys Gln Lys  
                     50                    55                    60

Gly Ile Glu Trp Lys Asp Asp Thr Leu Phe Glu Tyr Leu Glu Asn Pro  
                     65                    70                    75                    80

Lys Lys Tyr Ile Pro Gly Thr Lys Met Ala Phe Gly Gly Leu Lys Lys  
                     85                    90                    95

Pro Lys Asp Arg Asn Asp Leu Ile Thr Phe Leu Glu Glu Glu Thr Lys  
                     100                    105                    110

<210> 39  
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<400> 39  
 atg gca ccg aca cca tct tct tca aga tca aat caa act caa tac acc 48  
 Met Ala Pro Thr Pro Ser Ser Ser Arg Ser Asn Gln Thr Gln Tyr Thr  
   1                  5                  10                  15

tta atc aga act cca caa aca aaa caa cgt ctc aat ttc cac tca aaa 96  
 Leu Ile Arg Thr Pro Gln Thr Lys Gln Arg Leu Asn Phe His Ser Lys  
                   20                  25                  30

acc cca aac cca gac gga tct aaa gat cca tct cca ccg gag cat cca 144  
 Thr Pro Asn Pro Asp Gly Ser Lys Asp Pro Ser Pro Pro Glu His Pro  
           35                  40                  45



gtt gaa gta atc ggc cgg atc cga gat tac cct gac cgg aaa gag aaa 192  
 Val Glu Val Ile Gly Arg Ile Arg Asp Tyr Pro Asp Arg Lys Glu Lys  
 50 55 60

tca cct tcg atc tta caa gtc aac aca gat aat caa acg gta cga gtc 240  
 Ser Pro Ser Ile Leu Gln Val Asn Thr Asp Asn Gln Thr Val Arg Val  
 65 70 75 80

aga gct gat gtt ggg tac aga gac ttc aca ctc gac ggt gtt tct ttc 288  
 Arg Ala Asp Val Gly Tyr Arg Asp Phe Thr Leu Asp Gly Val Ser Phe  
 85 90 95

tcg gag caa gaa ggt ctt gaa gag ttc tac aag aag ttt ata gaa gag 336  
 Ser Glu Gln Glu Gly Leu Glu Glu Phe Tyr Lys Lys Phe Ile Glu Glu  
 100 105 110

agg att aaa gga gtg aaa gtt ggg aat aaa tgc acg att atg atg tat 384  
 Arg Ile Lys Gly Val Lys Val Gly Asn Lys Cys Thr Ile Met Met Tyr  
 115 120 125

gga cct act ggt gct gga aag agt cat act atg ttt ggt tgt ggg aaa 432  
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 Asn Glu Glu Ile Tyr Asp Leu Leu Ser Thr Asn Ser Ser Asn Asn Leu  
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 Met Gly Leu Val Met Arg Phe Asp Leu  
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 Tyr Leu Met Phe Val Met Leu Met Gly Leu Gly Phe Thr Ile Ser Asn  
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Ser Glu Asp Tyr Ser His Trp Ser His Arg Asn Arg Phe Gln Val Asn			
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Asp Thr Leu H			
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Gly Lys Asp Ser Val Leu Glu Val Thr Glu Gln Glu Tyr Asn Thr Cys			
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Asn Thr Thr His Pro Leu Thr Ser Leu Ser Asp Gly Asp Ser Leu Phe			
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Leu Leu Ser His Ser Gly Ser Tyr Phe Phe Ile Ser Gly Asn Ser Gln			
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Asn Cys Leu Lys Gly Gln Lys Leu Ala Val Lys Val Leu Ser Thr Val			
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His Gln Glu Leu Ser Ser Pro Gly Pro Ser Pro Gly Val Glu Pro Ser			
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Ser Asp Ser Asn Ser Arg Val Pro Ala Pro Gly Pro Ala Thr Ala Pro			
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Asn Ser Ala Gly Leu Val Gly Pro Gly Met Val Val Leu			
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85



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71.

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Ala Lys Gly Lys Asp Ser Val Leu Glu Val Thr Glu Gln Glu Tyr Asn
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Thr Cys Asn Thr Thr His Pro Leu Thr Ser Leu Ser Asp Gly Asp Ser
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Leu Phe Leu Leu Ser His Ser Gly Ser Tyr Phe Phe Ile Ser Gly Asn
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Ser Gln Asn Cys Leu Lys Gly Gln Lys Leu Ala Val Lys Val Leu Ser
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 Lys Val Gln Ala Val Leu Lys Ser Ile Lys Gln Ser Pro Lys Lys Val  
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 Ser Lys Arg Glu Arg Gln Leu Val Pro His Lys Leu Ile Glu Thr Ser  
 385 390 395 400  
 Pro Ile Trp Asn Arg Arg Gly Thr Lys Ala Asn His Arg Ser Ser Glu  
 405 410 415  
 Leu Val Leu Thr Ile Ile Leu Asp Val Thr Cys Val Gly Asn Met Glu  
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Lys Asn Arg Leu Asp Asn Leu Thr Asn Gln Asn Asn Ile Tyr His His  
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 Asn Pro Glu Glu Thr Cys Ser Phe Arg Cys Asn Gly Ser Glu Arg Ile  
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 Asp Val Asp Ala Asp Val Val Val Val Asp Val Val Glu Leu Leu Val  
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 ata agc aat tgc aat gtc ctc gca ttc tcc ggc atc aaa aca tcc ccg 148  
 Ile Ser Asn Cys Asn Val Leu Ala Phe Ser Gly Ile Lys Thr Ser Pro  
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 gaa acc gcc ttg gaa atc ttc gac gct tgg atc aaa act cct ttc aaa 196  
 Glu Thr Ala Leu Glu Ile Phe Asp Ala Trp Ile Lys Thr Pro Phe Lys  
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 Ser Phe Leu Asp Asn Ser Leu Ser Glu Met Ser Gln Ile Gly Lys Ser  
 75 80 85  
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 Thr Ala Gly Asp Ser Thr Lys Lys Ile Asp Glu Thr Thr Ala Ser  
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Cys Val Ile Cys Cys Leu Ala Lys Asn Arg Glu Phe Thr Pro Val Asp  
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 Ala Ile Val Arg Phe Lys Ala Gly Ser Val Glu Pro Ala His His His  
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 Thr Phe Gly His Asp Leu Val Val Ile Lys Gly Lys Lys Ser Val Trp  
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 Asn Leu Ser Lys Lys Glu Arg Ala Asp Leu Val Asp Gly Asp Tyr Leu  
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 Glu Phe Phe Ile Thr Trp Asp Gly His Trp Asp Ile Phe Leu Asp Glu  
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 35 40 45  
 Asp Ala Trp Ile Lys Thr Pro Phe Lys Ser Pro Cys Pro Ala Ser Gly  
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 Ser Glu Pro Trp Ser Ser Val Ile Ser Ser Phe Leu Asp Asn Ser Leu  
 65 70 75 80  
 Ser Glu Met Ser Gln Ile Gly Lys Ser Thr Ala Gly Asp Ser Thr Thr  
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Lys Lys Ile Asp Glu Thr Thr Ala Ser Cys Val Ile Cys Cys Leu Ala  
100 105 110

Lys Asn Arg Glu Phe Thr Pro Val Asp Ile Met Pro Gly Gly Ser Met  
115 120 125

Lys Ile Val Arg Glu Thr Pro Thr Ser Ala Ile Val Arg Phe Lys Ala  
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Gly Ser Val Glu Pro Ala His His His Thr Phe Gly His Asp Leu Val  
145 150 155 160

Val Ile Lys Gly Lys Lys Ser Val Trp Asn Leu Ser Lys Lys Glu Arg  
165 170 175

Ala Asp Leu Val Asp Gly Asp Tyr Leu Phe Thr Pro Ala Gly Asp Val  
180 185 190

His Arg Val Lys Tyr His Glu Asp Thr Glu Phe Phe Ile Thr Trp Asp  
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Pro Ile Ser Ser Thr Leu Asn Gln His Leu Val Asp Tyr Pro Thr Pro  
15 20 25

agc aat ctt agt tat tgg tgg ggg ttc ggt ccg tta gct ggt att tgt 146  
Ser Asn Leu Ser Tyr Trp Trp Gly Phe Gly Pro Leu Ala Gly Ile Cys  
30 35 40 45

tta gtc att cag ata gtg act ggc gtt ttt tta gct atg cat tac aca 194  
Leu Val Ile Gln Ile Val Thr Gly Val Phe Leu Ala Met His Tyr Thr  
50 55 60

cct cat gtg gat tta gct ttc aac agc gta gaa cac att atg aga gat 242

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Val	Glu	Gly	Gly	Trp	Leu	Leu	Arg	Tyr	Met	His	Ala	Asn	Gly	Ala	Ser		
		80					85					90					
atg	ttt	ctt	att	gtg	gtt	tac	ctt	cat	att	ttt	cgt	ggg	cta	tat	cat	338	
Met	Phe	Leu	Ile	Val	Val	Tyr	Leu	His	Ile	Phe	Arg	Gly	Leu	Tyr	His		
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gcg	agt	tat	agc	agt	cct	agg	gaa	ttt	gtt	tgg	tgt	ctt	gga	gtt	gta	386	
Ala	Ser	Tyr	Ser	Ser	Pro	Arg	Glu	Phe	Val	Trp	Cys	Leu	Gly	Val	Val		
110					115					120					125		
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Ile	Phe	Leu	Leu	Met	Ile	Val	Thr	Ala	Phe	Ile	Gly	Tyr	Val	Leu	Pro		
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tgg	ggg	cag	atg	agc	ttt	tgg	gga	gct	aca	gta	att	aca	agc	tta	gct	482	
Trp	Gly	Gln	Met	Ser	Phe	Trp	Gly	Ala	Thr	Val	Ile	Thr	Ser	Leu	Ala		
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Gly	Phe	Ser	Val	Asp	Asn	Ala	Thr	Leu	Asn	Arg	Phe	Phe	Ser	Leu	His		
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His	Leu	Leu	Pro	Phe	Ile	Leu	Val	Gly	Ala	Ser	Leu	Leu	His	Leu	Ala		
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Pro	Asn	Val	Leu	Gly	His	Pro	Asp	Asn	Tyr	Ile	Pro	Ala	Asn	Pro	Met		
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Ala	Ile	Leu	Arg	Ser	Ile	Pro	Asp	Lys	Ala	Gly	Gly	Val	Ala	Ala	Ile		

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tat gtg cgt agt tca agt ttt cga ccg att cac caa gga atg ttt tgg			1010
Tyr Val Arg Ser Ser Ser Phe Arg Pro Ile His Gln Gly Met Phe Trp			
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Leu Leu Leu Ala Asp Cys Leu Leu Leu Gly Trp Ile Gly Cys Gln Pro			
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gtg gag gct cca ttt gtt act att gga caa att tct cct ttg gtt ttc			1106
Val Glu Ala Pro Phe Val Thr Ile Gly Gln Ile Ser Pro Leu Val Phe			
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Phe Leu Phe Phe Ala Ile Thr Pro Ile Leu Gly Arg Val Gly Arg Gly			
370	375	380	
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35 40 45

Gln Ile Val Thr Gly Val Phe Leu Ala Met His Tyr Thr Pro His Val
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Asp Leu Ala Phe Asn Ser Val Glu His Ile Met Arg Asp Val Glu Gly
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100 105 110

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115 120 125

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 Pro Val Val Gly Asp Thr Ile Val Thr Trp Leu Trp Gly Gly Phe Ser  
 165 170 175  
 Val Asp Asn Ala Thr Leu Asn Arg Phe Phe Ser Leu His His Leu Leu  
 180 185 190  
 Pro Phe Ile Leu Val Gly Ala Ser Leu Leu His Leu Ala Ala Leu His  
 195 200 205  
 Gln Tyr Gly Ser Asn Asn Pro Leu Gly Val His Ser Glu Met Asp Lys  
 210 215 220  
 Ile Ala Phe Tyr Pro Tyr Phe Tyr Val Lys Asp Leu Val Gly Trp Val  
 225 230 235 240  
 Ala Phe Ala Ile Phe Phe Ser Ile Trp Ile Phe Tyr Ala Pro Asn Val  
 245 250 255  
 Leu Gly His Pro Asp Asn Tyr Ile Pro Ala Asn Pro Met Ser Thr Pro  
 260 265 270  
 Pro His Ile Val Pro Glu Trp Tyr Phe Leu Pro Ile His Ala Ile Leu  
 275 280 285  
 Arg Ser Ile Pro Asp Lys Ala Gly Gly Val Ala Ala Ile Ala Pro Val  
 290 295 300  
 Phe Ile Cys Leu Leu Ala Leu Pro Phe Phe Lys Ser Met Tyr Val Arg  
 305 310 315 320  
 Ser Ser Ser Phe Arg Pro Ile His Gln Gly Met Phe Trp Leu Leu Leu  
 325 330 335  
 Ala Asp Cys Leu Leu Leu Gly Trp Ile Gly Cys Gln Pro Val Glu Ala  
 340 345 350  
 Pro Phe Val Thr Ile Gly Gln Ile Ser Pro Leu Val Phe Phe Leu Phe  
 355 360 365  
 Phe Ala Ile Thr Pro Ile Leu Gly Arg Val Gly Arg Gly Ile Pro Asn  
 370 375 380  
 Ser Tyr Thr Asp Glu Thr Asp His Thr  
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&lt;210&gt; 47

&lt;211&gt; 1194

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1194)

&lt;400&gt; 47

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cga	gga	aat	tac	gca	gct	aca	ctc	gat	gtg	tcg	tat	ccg	gta	ttc	ccg	96
Arg	Gly	Asn	Tyr	Ala	Ala	Thr	Leu	Asp	Val	Ser	Tyr	Pro	Val	Phe	Pro	
			20					25					30			
caa	aat	aaa	gat	ggc	cgt	gca	ctt	cag	aaa	gtt	ctc	gga	acc	att	cgt	144
Gln	Asn	Lys	Asp	Gly	Arg	Ala	Leu	Gln	Lys	Val	Leu	Gly	Thr	Ile	Arg	
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Asn	Gly	Asp	Leu	Ala	Val	Ser	Ala	Pro	Lys	Thr	Ser	Leu	Arg	Ala	Gly	
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Ile	Phe	Gly	Glu	Gly	Ser	Ser	Leu	Val	Asp	Gln	Met	Pro	Cys	Lys	Val	
	65				70					75					80	
tac	gtg	gcg	ttc	cac	aaa	gaa	tca	tac	tgc	tcg	ctt	acc	ggg	cta	agc	288
Tyr	Val	Ala	Phe	His	Lys	Glu	Ser	Tyr	Cys	Ser	Leu	Thr	Gly	Leu	Ser	
				85					90					95		
aaa	cgc	gga	gtc	gca	ata	aac	gaa	gca	agt	ctt	tcc	ctg	gtc	gga	atc	336
Lys	Arg	Gly	Val	Ala	Ile	Asn	Glu	Ala	Ser	Leu	Ser	Leu	Val	Gly	Ile	
			100					105					110			
act	aaa	gtt	aga	gcc	ccc	gtc	gga	aat	acc	gtt	gga	gcg	gaa	gca	acc	384
Thr	Lys	Val	Arg	Ala	Pro	Val	Gly	Asn	Thr	Val	Gly	Ala	Glu	Ala	Thr	
		115					120					125				
gta	tac	ata	ggt	agt	cca	aaa	cct	tat	aca	gag	tgt	agt	act	cca	aat	432
Val	Tyr	Ile	Gly	Ser	Pro	Lys	Pro	Tyr	Thr	Glu	Cys	Ser	Thr	Pro	Asn	
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Lys	Met	Tyr	Ala	Val	Ala	Ala	Gly	Phe	Lys	Val	Ala	Ser	Phe	Ala	Ala	
	145				150					155				160		
agt	acg	tgc	gta	cgt	ccg	cct	gca	cgt	gca	cgt	cgt	acg	ctg	acc	gtg	528
Ser	Thr	Cys	Val	Arg	Pro	Pro	Ala	Arg	Ala	Arg	Arg	Thr	Leu	Thr	Val	
				165				170						175		
acg	tcg	acc	gtg	acg	ctg	tct	atg	gca	act	ggt	aaa	tgc	gta	aat	aca	576
Thr	Ser	Thr	Val	Thr	Leu	Ser	Met	Ala	Thr	Gly	Lys	Cys	Val	Asn	Thr	
			180					185					190			
gga	aac	gaa	cca	gta	tct	aaa	cct	aca	gga	gta	cgt	atg	atg	tta	att	624
Gly	Asn	Glu	Pro	Val	Ser	Lys	Pro	Thr	Gly	Val	Arg	Met	Met	Leu	Ile	
		195					200					205				



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cct ctc gat gct act ctc att aaa gta tgg act ggg gaa gta aaa aaa 672
Pro Leu Asp Ala Thr Leu Ile Lys Val Trp Thr Gly Glu Val Lys Lys
210 215 220

gcg ata gtt tcc cgg cct gca aaa att ttc aat agc gta gga aat tta 720
Ala Ile Val Ser Arg Pro Ala Lys Ile Phe Asn Ser Val Gly Asn Leu
225 230 235 240

gaa cgt cct tca att tcg cat tct tgt gga caa ggt ttg gat gaa gct 768
Glu Arg Pro Ser Ile Ser His Ser Cys Gly Gln Gly Leu Asp Glu Ala
245 250 255

gcc gct tat atc aag ggt aga ctt tct cca atc gtt aaa gca gaa aga 816
Ala Ala Tyr Ile Lys Gly Arg Leu Ser Pro Ile Val Lys Ala Glu Arg
260 265 270

att aaa gtt ttg gtt aaa gac gag cac gaa gaa gta aaa gaa ctt ctt 864
Ile Lys Val Leu Val Lys Asp Glu His Glu Glu Val Lys Glu Leu Leu
275 280 285

caa gaa ggt tac gaa gaa atc gtc ggt gag tct cca agt ttc aat tta 912
Gln Glu Gly Tyr Glu Glu Ile Val Gly Glu Ser Pro Ser Phe Asn Leu
290 295 300

gca caa gaa gcg tgg gaa aaa gct gaa aga cga gca aaa ggt cag tcc 960
Ala Gln Glu Ala Trp Glu Lys Ala Glu Arg Arg Ala Lys Gly Gln Ser
305 310 315 320

ccg tgc agt gcg gca aaa gca aac ctt gca acc tac tat ttt tca aca 1008
Pro Cys Ser Ala Ala Lys Ala Asn Leu Ala Thr Tyr Tyr Phe Ser Thr
325 330 335

ggg gat ttc gaa aaa tca att aaa ctc tac gaa gaa cct atg ggt ttg 1056
Gly Asp Phe Glu Lys Ser Ile Lys Leu Tyr Glu Glu Pro Met Gly Leu
340 345 350

aaa gat act gat aag agc tat ctg cga gaa cgt aga aaa aga gta gag 1104
Lys Asp Thr Asp Lys Ser Tyr Leu Arg Glu Arg Arg Lys Arg Val Glu
355 360 365

gct act acg ttg cgt gca ccg ttc gtg gtc cag ctg acc gtg cgt agt 1152
Ala Thr Thr Leu Arg Ala Pro Phe Val Val Gln Leu Thr Val Arg Ser
370 375 380

cgt acg acg atg atc gcc gtt ggt gaa agc aac gca aac tga 1194
Arg Thr Thr Met Ile Ala Val Gly Glu Ser Asn Ala Asn
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&lt;210&gt; 48

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 48

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Gln Asn Lys Asp Gly Arg Ala Leu Gln Lys Val Leu Gly Thr Ile Arg	35	40	45
Asn Gly Asp Leu Ala Val Ser Ala Pro Lys Thr Ser Leu Arg Ala Gly	50	55	60
Ile Phe Gly Glu Gly Ser Ser Leu Val Asp Gln Met Pro Cys Lys Val	65	70	75
Tyr Val Ala Phe His Lys Glu Ser Tyr Cys Ser Leu Thr Gly Leu Ser	85	90	95
Lys Arg Gly Val Ala Ile Asn Glu Ala Ser Leu Ser Leu Val Gly Ile	100	105	110
Thr Lys Val Arg Ala Pro Val Gly Asn Thr Val Gly Ala Glu Ala Thr	115	120	125
Val Tyr Ile Gly Ser Pro Lys Pro Tyr Thr Glu Cys Ser Thr Pro Asn	130	135	140
Lys Met Tyr Ala Val Ala Ala Gly Phe Lys Val Ala Ser Phe Ala Ala	145	150	155
Ser Thr Cys Val Arg Pro Pro Ala Arg Ala Arg Arg Thr Leu Thr Val	165	170	175
Thr Ser Thr Val Thr Leu Ser Met Ala Thr Gly Lys Cys Val Asn Thr	180	185	190
Gly Asn Glu Pro Val Ser Lys Pro Thr Gly Val Arg Met Met Leu Ile	195	200	205
Pro Leu Asp Ala Thr Leu Ile Lys Val Trp Thr Gly Glu Val Lys Lys	210	215	220
Ala Ile Val Ser Arg Pro Ala Lys Ile Phe Asn Ser Val Gly Asn Leu	225	230	235
Glu Arg Pro Ser Ile Ser His Ser Cys Gly Gln Gly Leu Asp Glu Ala	245	250	255
Ala Ala Tyr Ile Lys Gly Arg Leu Ser Pro Ile Val Lys Ala Glu Arg	260	265	270
Ile Lys Val Leu Val Lys Asp Glu His Glu Glu Val Lys Glu Leu Leu	275	280	285
Gln Glu Gly Tyr Glu Glu Ile Val Gly Glu Ser Pro Ser Phe Asn Leu	290	295	300
Ala Gln Glu Ala Trp Glu Lys Ala Glu Arg Arg Ala Lys Gly Gln Ser			

305                      310                      315                      320  
 Pro Cys Ser Ala Ala Lys Ala Asn Leu Ala Thr Tyr Tyr Phe Ser Thr  
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 Gly Asp Phe Glu Lys Ser Ile Lys Leu Tyr Glu Glu Pro Met Gly Leu  
                                  340                      345                      350  
 Lys Asp Thr Asp Lys Ser Tyr Leu Arg Glu Arg Arg Lys Arg Val Glu  
                                  355                      360                      365  
 Ala Thr Thr Leu Arg Ala Pro Phe Val Val Gln Leu Thr Val Arg Ser  
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 Arg Thr Thr Met Ile Ala Val Gly Glu Ser Asn Ala Asn  
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 gtc gtc ttt tcc gtc gcg ctt ctt ctg ttc tac ttc tct gaa act tct 97  
 Val Val Phe Ser Val Ala Leu Leu Leu Phe Tyr Phe Ser Glu Thr Ser  
                                  20                      25                      30  
  
 cta gga gct cct tgt ccc atc aat ggc ttg cca atc gtg agg aat att 145  
 Leu Gly Ala Pro Cys Pro Ile Asn Gly Leu Pro Ile Val Arg Asn Ile  
                                  35                      40                      45  
  
 agt gac ctt cct cag gat aac tat gga aga cca ggt ctt tcc cac atg 193  
 Ser Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met  
                                  50                      55                      60  
  
 act gtt gct ggc tcc gta ttg cat gga atg aaa gag gtt gaa ata tgg 241  
 Thr Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp  
                                  65                      70                      75  
  
 ctt cag aca ttt gct cca ggt tca gag aca cca att cac agg cac tcc 289  
 Leu Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser  
                                  80                      85                      90                      95  
  
 tgt gaa gag gtt ttt gtt gtc cta aag ggc agt ggt act ctg tat ctc 337  
 Cys Glu Glu Val Phe Val Val Leu Lys Gly Ser Gly Thr Leu Tyr Leu  
                                  100                      105                      110

gct gaa aca cat gga aat ttc cct ggg aaa cca atc gaa ttt cca atc 385  
 Ala Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile  
                   115                  120                  125

ttt gcc aac agt aca att cat att ccg atc aat gat gct cat cag gtc 433  
 Phe Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val  
                   130                  135                  140

aaa aac acc ggt cat gag gac ctg cag gtg ttg gtt atc ata tct cgg 481  
 Lys Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg  
                   145                  150                  155

ccg cct att aaa atc ttc atc tac gaa gac tgg ttt atg cca cac act 529  
 Pro Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr  
                   160                  165                  170                  175

gct gca agg ctg aag ttc cct tac tat tgg gat gag caa tgc att caa 577  
 Ala Ala Arg Leu Lys Phe Pro Tyr Tyr Trp Asp Glu Gln Cys Ile Gln  
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                   20                  25                  30

Gly Ala Pro Cys Pro Ile Asn Gly Leu Pro Ile Val Arg Asn Ile Ser  
                   35                  40                  45

Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met Thr  
                   50                  55                  60

Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp Leu  
                   65                  70                  75                  80

Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser Cys  
                   85                  90                  95

Glu Glu Val Phe Val Val Leu Lys Gly Ser Gly Thr Leu Tyr Leu Ala  
                   100                  105                  110

Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile Phe  
                   115                  120                  125

Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val Lys  
                   130                  135                  140

Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg Pro  
 145 150 155 160

Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr Ala  
 165 170 175

Ala Arg Leu Lys Phe Pro Tyr Tyr Trp Asp Glu Gln Cys Ile Gln Glu  
 180 185 190

Ser Gln Lys Asp Glu Leu  
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cca tgt aga ggc gcg tca atc act gga tct cta cgt gac cgt cga ccg 96  
 Pro Cys Arg Gly Ala Ser Ile Thr Gly Ser Leu Arg Asp Arg Arg Pro  
 20 25 30

acc gct atc ctt atc gga acc ctc acc gct tta ggc ggt gga gtt aga 144  
 Thr Ala Ile Leu Ile Gly Thr Leu Thr Ala Leu Gly Gly Gly Val Arg  
 35 40 45

tgt ggc tct tgc ccc agt gtc gac cgt tgc gga cac gca agt gcc gcc 192  
 Cys Gly Ser Cys Pro Ser Val Asp Arg Cys Gly His Ala Ser Ala Ala  
 50 55 60

ata gcg cgt gat agc tgt gcc gtg ttc gca tgg aag cga ggt acg cga 240  
 Ile Ala Arg Asp Ser Cys Ala Val Phe Ala Trp Lys Arg Gly Thr Arg  
 65 70 75 80

caa gag tac tgg tgc tcg act gaa ccg acc ctt gac tgg ggc ccc ggt 288  
 Gln Glu Tyr Trp Cys Ser Thr Glu Pro Thr Leu Asp Trp Gly Pro Gly  
 85 90 95

ggt gga ccc gac ttc gat tgt gat gat ggt ggt gac gat ccg ctt ttg 336  
 Gly Gly Pro Asp Phe Asp Cys Asp Asp Gly Gly Asp Asp Pro Leu Leu  
 100 105 110

att caa gat ggc gta aaa gct gcg gag gaa tat gct aaa tct gga aaa 384  
 Ile Gln Asp Gly Val Lys Ala Ala Glu Glu Tyr Ala Lys Ser Gly Lys  
 115 120 125

gtt cca gat cca agc tgt act gat aat gct gag ttt caa gtt gtg ctt	432
Val Pro Asp Pro Ser Cys Thr Asp Asn Ala Glu Phe Gln Val Val Leu	
130 135 140	
att att att agg gag ggg ttg aaa act gat cct tta aaa tac act aag	480
Ile Ile Ile Arg Glu Gly Leu Lys Thr Asp Pro Leu Lys Tyr Thr Lys	
145 150 155 160	
cga ccc agt tgc ctt gtt ggt gtt tct gag gaa act act act ggt gtt	528
Arg Pro Ser Cys Leu Val Gly Val Ser Glu Glu Thr Thr Thr Gly Val	
165 170 175	
aag aga agt tac caa atg cag ccg aaa tgt act ttg ctt ttg cat gct	576
Lys Arg Ser Tyr Gln Met Gln Pro Lys Cys Thr Leu Leu Leu His Ala	
180 185 190	
act gat gtt tgt gac acc gtg atc aag agc aag att gat aac ttg tac	624
Thr Asp Val Cys Asp Thr Val Ile Lys Ser Lys Ile Asp Asn Leu Tyr	
195 200 205	
gga tgc cgc cac tca ctt tcg gat ggt ctc atg agg gct act gat gtt	672
Gly Cys Arg His Ser Leu Ser Asp Gly Leu Met Arg Ala Thr Asp Val	
210 215 220	
cgt cgc ccc tgc aag gta gcg ctt gta ggc ggt tac gga gat gtc ttt	720
Arg Arg Pro Cys Lys Val Ala Leu Val Gly Gly Tyr Gly Asp Val Phe	
225 230 235 240	
aag ggt tgg gtt gct gcc ttg aag caa gct ggt gca cgt gtc atc gtg	768
Lys Gly Trp Val Ala Ala Leu Lys Gln Ala Gly Ala Arg Val Ile Val	
245 250 255	
act gag atc ccg caa atc tgt gcc gtc caa gct acc atg gaa ggt agt	816
Thr Glu Ile Pro Gln Ile Cys Ala Val Gln Ala Thr Met Glu Gly Ser	
260 265 270	
tcg gtc ctt acc ctt gag gat gtc gtt tca gat gtt gat cgc ttc gtt	864
Ser Val Leu Thr Leu Glu Asp Val Val Ser Asp Val Asp Arg Phe Val	
275 280 285	
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Thr Thr Thr Gly Asn Lys Asp Leu Ile Met Val Asp His Met Arg Arg	
290 295 300	
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Met Lys Asn Gln Ala Ile Val Cys Asn Ile Arg Arg Phe Asp Asn Glu	
305 310 315 320	
atc gac atg cgc agt ctc gag acc ttc cct gga gtg aag cgg atc aca	1008
Ile Asp Met Arg Ser Leu Glu Thr Phe Pro Gly Val Lys Arg Ile Thr	
325 330 335	
atc aag gcc cag act gac aga tgg gtc ttt cgc gac acc aac aga ggt	1056
Ile Lys Ala Gln Thr Asp Arg Trp Val Phe Arg Asp Thr Asn Arg Gly	
340 345 350	
atc att gtc cca gcc gag ggg cgt ctc atg acg atg gga tgc gcc act	1104



Ile Ile Val Pro Ala Glu Gly Arg Leu Met Thr Met Gly Cys Ala Thr  
 355 360 365  
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 Gly His Pro Ser Phe Arg Thr Ser Cys Ser Phe Thr Asn Gln Val Ser  
 370 375 380  
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 Ser Gln Leu Glu Leu Trp Arg Glu Lys Ser Thr Gly Lys Tyr Glu Lys  
 385 390 395 400  
 aaa gtg tac gtc ttc cca aag cac ctt gag aag aag gtt gcc gcc ctt 1248  
 Lys Val Tyr Val Phe Pro Lys His Leu Glu Lys Lys Val Ala Ala Leu  
 405 410 415  
 cat ctc gta aag ctc gga gca agg ctc act aag ctt agt cgg tgc acg 1296  
 His Leu Val Lys Leu Gly Ala Arg Leu Thr Lys Leu Ser Arg Cys Thr  
 420 425 430  
 ttg ttg tgc acg gac gac cca gtt gaa ggt cgt aaa gag cct cct cac 1344  
 Leu Leu Cys Thr Asp Asp Pro Val Glu Gly Arg Lys Glu Pro Pro His  
 435 440 445  
 cgt gct ggc agc cct gaa ccg tgc cag ctg cag ctg acc gtg ttc agg 1392  
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 35 40 45  
 Cys Gly Ser Cys Pro Ser Val Asp Arg Cys Gly His Ala Ser Ala Ala  
 50 55 60  
 Ile Ala Arg Asp Ser Cys Ala Val Phe Ala Trp Lys Arg Gly Thr Arg  
 65 70 75 80  
 Gln Glu Tyr Trp Cys Ser Thr Glu Pro Thr Leu Asp Trp Gly Pro Gly  
 85 90 95  
 Gly Gly Pro Asp Phe Asp Cys Asp Asp Gly Gly Asp Asp Pro Leu Leu

100					105					110					
Ile	Gln	Asp	Gly	Val	Lys	Ala	Ala	Glu	Glu	Tyr	Ala	Lys	Ser	Gly	Lys
		115					120					125			
Val	Pro	Asp	Pro	Ser	Cys	Thr	Asp	Asn	Ala	Glu	Phe	Gln	Val	Val	Leu
		130					135					140			
Ile	Ile	Ile	Arg	Glu	Gly	Leu	Lys	Thr	Asp	Pro	Leu	Lys	Tyr	Thr	Lys
							150					155			
Arg	Pro	Ser	Cys	Leu	Val	Gly	Val	Ser	Glu	Glu	Thr	Thr	Thr	Gly	Val
							165					170			
Lys	Arg	Ser	Tyr	Gln	Met	Gln	Pro	Lys	Cys	Thr	Leu	Leu	Leu	His	Ala
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							200					205			
Gly	Cys	Arg	His	Ser	Leu	Ser	Asp	Gly	Leu	Met	Arg	Ala	Thr	Asp	Val
							215					220			
Arg	Arg	Pro	Cys	Lys	Val	Ala	Leu	Val	Gly	Gly	Tyr	Gly	Asp	Val	Phe
							230					235			
Lys	Gly	Trp	Val	Ala	Ala	Leu	Lys	Gln	Ala	Gly	Ala	Arg	Val	Ile	Val
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Thr	Glu	Ile	Pro	Gln	Ile	Cys	Ala	Val	Gln	Ala	Thr	Met	Glu	Gly	Ser
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Ser	Val	Leu	Thr	Leu	Glu	Asp	Val	Val	Ser	Asp	Val	Asp	Arg	Phe	Val
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Met	Lys	Asn	Gln	Ala	Ile	Val	Cys	Asn	Ile	Arg	Arg	Phe	Asp	Asn	Glu
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Ile	Asp	Met	Arg	Ser	Leu	Glu	Thr	Phe	Pro	Gly	Val	Lys	Arg	Ile	Thr
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Ile	Lys	Ala	Gln	Thr	Asp	Arg	Trp	Val	Phe	Arg	Asp	Thr	Asn	Arg	Gly
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Ile	Ile	Val	Pro	Ala	Glu	Gly	Arg	Leu	Met	Thr	Met	Gly	Cys	Ala	Thr
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Gly	His	Pro	Ser	Phe	Arg	Thr	Ser	Cys	Ser	Phe	Thr	Asn	Gln	Val	Ser
							370					375			
Ser	Gln	Leu	Glu	Leu	Trp	Arg	Glu	Lys	Ser	Thr	Gly	Lys	Tyr	Glu	Lys
							385					390			
Lys	Val	Tyr	Val	Phe	Pro	Lys	His	Leu	Glu	Lys	Lys	Val	Ala	Ala	Leu

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His Leu Val Lys Leu Gly Ala Arg Leu Thr Lys Leu Ser Arg Cys Thr		
420	425	430
Leu Leu Cys Thr Asp Asp Pro Val Glu Gly Arg Lys Glu Pro Pro His		
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Arg Ala Gly Ser Pro Glu Pro Cys Gln Leu Gln Leu Thr Val Phe Arg		
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Asp Val Asp Glu Ile Val Arg Leu Arg Lys Arg Phe Phe Lys Leu Asp	
20                      25                      30	
aga gat tgt tca gga tca gaa ctt gga agt gag ttc atg agt ttg cct	144
Arg Asp Cys Ser Gly Ser Glu Leu Gly Ser Glu Phe Met Ser Leu Pro	
35                      40                      45	
caa gtt agt tcg aac cct ctt cgg atg cgt gag atg cgt aat ttc gat	192
Gln Val Ser Ser Asn Pro Leu Arg Met Arg Glu Met Arg Asn Phe Asp	
50                      55                      60	
aat gat tgc gta ggg agt gtg gat ttt atc gag ttc atc aat gga cgt	240
Asn Asp Cys Val Gly Ser Val Asp Phe Ile Glu Phe Ile Asn Gly Arg	
65                      70                      75                      80	
tcc agt ttc agt act gtc ggg cag aag aat gct aaa ttg aga ttt gca	288
Ser Ser Phe Ser Thr Val Gly Gln Lys Asn Ala Lys Leu Arg Phe Ala	
85                      90                      95	
ccg att atc tat gat tgc gat aaa gat gga cct ata tca aac ggt gag	336
Pro Ile Ile Tyr Asp Cys Asp Lys Asp Gly Pro Ile Ser Asn Gly Glu	
100                      105                      110	
tta ttt agg gtg ttg cgt att atg gtt cat gac aat ctg agt gat aat	384
Leu Phe Arg Val Leu Arg Ile Met Val His Asp Asn Leu Ser Asp Asn	
115                      120                      125	
cag ctg cag cag cgt tgc gat tgc acg cgt agt ggc gga gat aat gac	432
Gln Leu Gln Gln Arg Cys Asp Cys Thr Arg Ser Gly Gly Asp Asn Asp	

130 135 140  
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 Gly Asp Gly Arg Gly Ala Lys Asn Ser Phe Glu Glu Phe Tyr Gly Arg  
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 Leu Pro Ala Thr Val Arg Arg Arg Pro Tyr Arg Thr Leu Val Ser Gly  
 165 170 175  
 gat gtg taa agttcagtgc accgtgaccg tgagcctgga agcctgaacg 577  
 Asp Val  
 ctgacaagcc cttaagccaa aaaattggct gaggcctgat gccctgagat gccaaaggct 637  
 ttttaggctt ttagagaaaa aggctaaaaa aaaggctaga aaaaaaggct cttaggcctg 697  
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 Arg Asp Cys Ser Gly Ser Glu Leu Gly Ser Glu Phe Met Ser Leu Pro  
 35 40 45  
 Gln Val Ser Ser Asn Pro Leu Arg Met Arg Glu Met Arg Asn Phe Asp  
 50 55 60  
 Asn Asp Cys Val Gly Ser Val Asp Phe Ile Glu Phe Ile Asn Gly Arg  
 65 70 75 80  
 Ser Ser Phe Ser Thr Val Gly Gln Lys Asn Ala Lys Leu Arg Phe Ala  
 85 90 95  
 Pro Ile Ile Tyr Asp Cys Asp Lys Asp Gly Pro Ile Ser Asn Gly Glu  
 100 105 110  
 Leu Phe Arg Val Leu Arg Ile Met Val His Asp Asn Leu Ser Asp Asn  
 115 120 125  
 Gln Leu Gln Gln Arg Cys Asp Cys Thr Arg Ser Gly Gly Asp Asn Asp  
 130 135 140  
 Gly Asp Gly Arg Gly Ala Lys Asn Ser Phe Glu Glu Phe Tyr Gly Arg  
 145 150 155 160

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Asp Val

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tgg gcg gtg aac ccc tgc ttc att gct tcc tgt tcc tgt ctc ctc gtt 99  
 Trp Ala Val Asn Pro Cys Phe Ile Ala Ser Cys Ser Cys Leu Leu Val  
 15 20 25 30

ggc ttc ggc gac gca atc ttc tac gag tgc ttc gcc ggg gat ttt gat 147  
 Gly Phe Gly Asp Ala Ile Phe Tyr Glu Ser Phe Ala Gly Asp Phe Asp  
 35 40 45

gca cgc tgg att tta tcc ggc tca aag tgt ctc tgc gat tgc gcc aag 195  
 Ala Arg Trp Ile Leu Ser Gly Ser Lys Cys Leu Ser Asp Ser Ala Lys  
 50 55 60

aat gct ggg ttt gat gat tat gga ctt ctt gtg ggt gaa caa gcc agg 243  
 Asn Ala Gly Phe Asp Asp Tyr Gly Leu Leu Val Gly Glu Gln Ala Arg  
 65 70 75

aag cct cct ata gtc aag gaa ctt gcc gag tct ctc agt cta aag gac 291  
 Lys Pro Pro Ile Val Lys Glu Leu Ala Glu Ser Leu Ser Leu Lys Asp  
 80 85 90

gga aga gtt gtt ctt gag tgt gag act cgc ctt gac cat ggc atc gac 339  
 Gly Arg Val Val Leu Glu Cys Glu Thr Arg Leu Asp His Gly Ile Asp  
 95 100 105 110

tgt gga ggt ccc tgt att aga tat ctt cga acc cag gag agc gga tgg 387  
 Cys Gly Gly Pro Cys Ile Arg Tyr Leu Arg Thr Gln Glu Ser Gly Trp  
 115 120 125

aaa ttt gac agc tcc acc atg ttt ggt gct gct aag tat ggc gcg agg 435  
 Lys Phe Asp Ser Ser Thr Met Phe Gly Ala Ala Lys Tyr Gly Ala Arg  
 130 135 140

agg acc cag ttc ttc ggg ggc cac ccc cag aac cca aac agt ggt gag 483  
 Arg Thr Gln Phe Phe Gly Gly His Pro Gln Asn Pro Asn Ser Gly Glu  
 145 150 155

tgt gtt gac cat gat cac aac cag cgg gct tcc ctc aca tcg gac aaa	531
Cys Val Asp His Asp His Asn Gln Arg Ala Ser Leu Thr Ser Asp Lys	
160 165 170	
gta cct cgt ttg tac act gga att ctg tcg ccc gaa aat gaa ttc cag	579
Val Pro Arg Leu Tyr Thr Gly Ile Leu Ser Pro Glu Asn Glu Phe Gln	
175 180 185 190	
atc ttg ata gat cgg ggg ttg gag acc aag gcc aaa atc ttc cct tgt	627
Ile Leu Ile Asp Arg Gly Leu Glu Thr Lys Ala Lys Ile Phe Pro Cys	
195 200 205	
gag gac ttt gag cct cct gtt ata cca tcc aag aga agc cct gat aat	675
Glu Asp Phe Glu Pro Pro Val Ile Pro Ser Lys Arg Ser Pro Asp Asn	
210 215 220	
ccg tcg aag cgg act gag gac tcg gac gaa aaa gcc aaa atc cca ggc	723
Pro Ser Lys Arg Thr Glu Asp Ser Asp Glu Lys Ala Lys Ile Pro Gly	
225 230 235	
cca agt gcc ctg aag cga cag gaa agc gat gag gat ccg aac cgg gaa	771
Pro Ser Ala Leu Lys Arg Gln Glu Ser Asp Glu Asp Pro Asn Arg Glu	
240 245 250	
atc tta cat gaa gaa gcc ggg aga cgt tcg tcc gat gtt ggg gcc cac	819
Ile Leu His Glu Glu Ala Gly Arg Arg Ser Ser Asp Val Gly Ala His	
255 260 265 270	
gca aaa gac cag gca cac gaa cct gag cca aaa cac tgg ggt gct gaa	867
Ala Lys Asp Gln Ala His Glu Pro Glu Pro Lys His Trp Gly Ala Glu	
275 280 285	
aag gat ggt gaa tgc gca ccc cca aag att gaa aac gca aag cgg ggg	915
Lys Asp Gly Glu Cys Ala Pro Pro Lys Ile Glu Asn Ala Lys Arg Gly	
290 295 300	
gcc gcc cct agt tgt ggt gta tcg gag agg caa acc aag att agt cca	963
Ala Ala Pro Ser Cys Gly Val Ser Glu Arg Gln Thr Lys Ile Ser Pro	
305 310 315	
aat tat aag gga aaa ccc tcc gtg ggt cca aac gtt tac caa ggg att	1011
Asn Tyr Lys Gly Lys Pro Ser Val Gly Pro Asn Val Tyr Gln Gly Ile	
320 325 330	
tgg aaa ccc cgc gag atg cta aac cct gga tcg ttc caa atc gca aaa	1059
Trp Lys Pro Arg Glu Met Leu Asn Pro Gly Ser Phe Gln Ile Ala Lys	
335 340 345 350	
ccc gct tgt gag cct att gct ggt ata ggc atg gag att agg aag cag	1107
Pro Ala Cys Glu Pro Ile Ala Gly Ile Gly Met Glu Ile Arg Lys Gln	
355 360 365	
ggc atc cta tta gac act gtg gtg ggg gtt agg ggg gat aca ggt gaa	1155
Gly Ile Leu Leu Asp Thr Val Val Gly Val Arg Gly Asp Thr Gly Glu	
370 375 380	



gaa tat ggg gaa acc ccg ttg aag acc acg tgt acc gtc gag aag cac 1203  
 Glu Tyr Gly Glu Thr Pro Leu Lys Thr Thr Cys Thr Val Glu Lys His  
 385 390 395  
 agt ttg cag gct caa gag gcg aga acc cgg tca gac gct ggt tca ccc 1251  
 Ser Leu Gln Ala Gln Glu Ala Arg Thr Arg Ser Asp Ala Gly Ser Pro  
 400 405 410  
 tac acc agg tac gta tct aaa atc ccc ggg aaa gcc gat aat ccc ttc 1299  
 Tyr Thr Arg Tyr Val Ser Lys Ile Pro Gly Lys Ala Asp Asn Pro Phe  
 415 420 425 430  
 tcg agc gag cac aaa tgt aag aat ttc gat ctg att gag gct gag aaa 1347  
 Ser Ser Glu His Lys Cys Lys Asn Phe Asp Leu Ile Glu Ala Glu Lys  
 435 440 445  
 cag tgt gcc aat gca gta atc ctg ggt gtt gtg gtt aac tcc ggt tca 1395  
 Gln Cys Ala Asn Ala Val Ile Leu Gly Val Val Val Asn Ser Gly Ser  
 450 455 460  
 att aac tcc gtt gtg tct tgg ggc tac aaa cct ggc acg gtg aac aag 1443  
 Ile Asn Ser Val Val Ser Trp Gly Tyr Lys Pro Gly Thr Val Asn Lys  
 465 470 475  
 aac caa gaa cgc aga gca ccc tcc cag cga cgt agt agc gag att gaa 1491  
 Asn Gln Glu Arg Arg Ala Pro Ser Gln Arg Arg Ser Ser Glu Ile Glu  
 480 485 490  
 gga acc caa gac cga cga aaa cag gat gtt ggc cga cgc caa gct gcc 1539  
 Gly Thr Gln Asp Arg Arg Lys Gln Asp Val Gly Arg Arg Gln Ala Ala  
 495 500 505 510  
 agc tcg ccc agg cgc tga taattaaatc cgatccgtcc tttaaccccc 1587  
 Ser Ser Pro Arg Arg  
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 35 40 45  
 Trp Ile Leu Ser Gly Ser Lys Cys Leu Ser Asp Ser Ala Lys Asn Ala  
 50 55 60

Gly Phe Asp Asp Tyr Gly Leu Leu Val Gly Glu Gln Ala Arg Lys Pro  
 65 70 75 80  
 Pro Ile Val Lys Glu Leu Ala Glu Ser Leu Ser Leu Lys Asp Gly Arg  
 85 90 95  
 Val Val Leu Glu Cys Glu Thr Arg Leu Asp His Gly Ile Asp Cys Gly  
 100 105 110  
 Gly Pro Cys Ile Arg Tyr Leu Arg Thr Gln Glu Ser Gly Trp Lys Phe  
 115 120 125  
 Asp Ser Ser Thr Met Phe Gly Ala Ala Lys Tyr Gly Ala Arg Arg Thr  
 130 135 140  
 Gln Phe Phe Gly Gly His Pro Gln Asn Pro Asn Ser Gly Glu Cys Val  
 145 150 155 160  
 Asp His Asp His Asn Gln Arg Ala Ser Leu Thr Ser Asp Lys Val Pro  
 165 170 175  
 Arg Leu Tyr Thr Gly Ile Leu Ser Pro Glu Asn Glu Phe Gln Ile Leu  
 180 185 190  
 Ile Asp Arg Gly Leu Glu Thr Lys Ala Lys Ile Phe Pro Cys Glu Asp  
 195 200 205  
 Phe Glu Pro Pro Val Ile Pro Ser Lys Arg Ser Pro Asp Asn Pro Ser  
 210 215 220  
 Lys Arg Thr Glu Asp Ser Asp Glu Lys Ala Lys Ile Pro Gly Pro Ser  
 225 230 235 240  
 Ala Leu Lys Arg Gln Glu Ser Asp Glu Asp Pro Asn Arg Glu Ile Leu  
 245 250 255  
 His Glu Glu Ala Gly Arg Arg Ser Ser Asp Val Gly Ala His Ala Lys  
 260 265 270  
 Asp Gln Ala His Glu Pro Glu Pro Lys His Trp Gly Ala Glu Lys Asp  
 275 280 285  
 Gly Glu Cys Ala Pro Pro Lys Ile Glu Asn Ala Lys Arg Gly Ala Ala  
 290 295 300  
 Pro Ser Cys Gly Val Ser Glu Arg Gln Thr Lys Ile Ser Pro Asn Tyr  
 305 310 315 320  
 Lys Gly Lys Pro Ser Val Gly Pro Asn Val Tyr Gln Gly Ile Trp Lys  
 325 330 335  
 Pro Arg Glu Met Leu Asn Pro Gly Ser Phe Gln Ile Ala Lys Pro Ala  
 340 345 350  
 Cys Glu Pro Ile Ala Gly Ile Gly Met Glu Ile Arg Lys Gln Gly Ile  
 355 360 365

Leu Leu Asp Thr Val Val Gly Val Arg Gly Asp Thr Gly Glu Glu Tyr  
 370 375 380  
 Gly Glu Thr Pro Leu Lys Thr Thr Cys Thr Val Glu Lys His Ser Leu  
 385 390 395 400  
 Gln Ala Gln Glu Ala Arg Thr Arg Ser Asp Ala Gly Ser Pro Tyr Thr  
 405 410 415  
 Arg Tyr Val Ser Lys Ile Pro Gly Lys Ala Asp Asn Pro Phe Ser Ser  
 420 425 430  
 Glu His Lys Cys Lys Asn Phe Asp Leu Ile Glu Ala Glu Lys Gln Cys  
 435 440 445  
 Ala Asn Ala Val Ile Leu Gly Val Val Val Asn Ser Gly Ser Ile Asn  
 450 455 460  
 Ser Val Val Ser Trp Gly Tyr Lys Pro Gly Thr Val Asn Lys Asn Gln  
 465 470 475 480  
 Glu Arg Arg Ala Pro Ser Gln Arg Arg Ser Ser Glu Ile Glu Gly Thr  
 485 490 495  
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 500 505 510  
 Pro Arg Arg  
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cgg gtg acc agg gac ggt tcg ggg ccc gga aaa acc ggt gtc aca cgc 99  
 Arg Val Thr Arg Asp Gly Ser Gly Pro Gly Lys Thr Gly Val Thr Arg  
 15 20 25

ggg tcg tca ccc atg cga tgg gca tgg aag cgg tgg caa gcc gtc ggg 147  
 Gly Ser Ser Pro Met Arg Trp Ala Trp Lys Arg Trp Gln Ala Val Gly  
 30 35 40 45

gca tcg acg gcc cgc acg tgg ttc ggg aca gag aac cag aaa gga ata 195  
 Ala Ser Thr Ala Arg Thr Trp Phe Gly Thr Glu Asn Gln Lys Gly Ile  
 50 55 60

acg	aca	agc	acc	cgc	gcg	cgg	cgc	tac	gcg	gtc	tcg	gcc	aaa	ttc	ccg	243
Thr	Thr	Ser	Thr	Arg	Ala	Arg	Arg	Tyr	Ala	Val	Ser	Ala	Lys	Phe	Pro	
			65					70					75			
aga	tta	agt	aat	aag	ggc	aaa	gat	tac	atg	cgt	tgc	gtc	ctc	caa	tac	291
Arg	Leu	Ser	Asn	Lys	Gly	Lys	Asp	Tyr	Met	Arg	Cys	Val	Leu	Gln	Tyr	
		80					85					90				
acc	gtc	aaa	aat	gaa	caa	aaa	gtt	gat	tgt	ggc	ggc	tca	tat	atc	aag	339
Thr	Val	Lys	Asn	Glu	Gln	Lys	Val	Asp	Cys	Gly	Gly	Ser	Tyr	Ile	Lys	
	95					100					105					
tta	tta	cct	tcg	aaa	ttg	cgc	acg	ggc	gat	ggc	gat	ggc	gtg	tca	gaa	387
Leu	Leu	Pro	Ser	Lys	Leu	Arg	Thr	Gly	Asp	Gly	Asp	Gly	Val	Ser	Glu	
110					115					120					125	
tat	tca	att	atg	ttt	ggc	cca	gat	tcg	aca	ggc	gca	tca	cgt	act	gtt	435
Tyr	Ser	Ile	Met	Phe	Gly	Pro	Asp	Ser	Thr	Gly	Ala	Ser	Arg	Thr	Val	
				130					135					140		
cgt	cga	gct	cgc	aat	tat	aag	ggc	aaa	cgg	cat	ttg	cgg	aaa	aaa	gaa	483
Arg	Arg	Ala	Arg	Asn	Tyr	Lys	Gly	Lys	Arg	His	Leu	Arg	Lys	Lys	Glu	
			145					150					155			
cag	aat	aaa	gtg	gaa	aca	gat	caa	tta	aca	cat	cag	tat	act	acg	agt	531
Gln	Asn	Lys	Val	Glu	Thr	Asp	Gln	Leu	Thr	His	Gln	Tyr	Thr	Thr	Ser	
		160					165					170				
tgg	tca	cca	gat	tgg	acc	tac	aac	gtt	cta	gta	gat	aat	aag	gaa	tcg	579
Trp	Ser	Pro	Asp	Trp	Thr	Tyr	Asn	Val	Leu	Val	Asp	Asn	Lys	Glu	Ser	
	175					180					185					
caa	gca	ggg	aac	ctt	gcc	gac	gac	tgc	gag	tta	ctt	cca	cag	aag	cga	627
Gln	Ala	Gly	Asn	Leu	Ala	Asp	Asp	Cys	Glu	Leu	Leu	Pro	Gln	Lys	Arg	
190					195				200						205	
atc	ttc	cga	ccc	agc	tgc	cga	aaa	caa	tcc	aaa	cca	gtc	acc	tgc	gta	675
Ile	Phe	Arg	Pro	Ser	Cys	Arg	Lys	Gln	Ser	Lys	Pro	Val	Thr	Cys	Val	
				210					215					220		
gac	gtc	aag	cac	cac	gcc	ccc	cga	cga	aat	gtg	aaa	ccc	gcc	ggg	cac	723
Asp	Val	Lys	His	His	Ala	Pro	Arg	Arg	Asn	Val	Lys	Pro	Ala	Gly	His	
			225					230					235			
gat	gac	att	cca	gcg	cga	cgg	acg	acg	ccg	gaa	gcg	gtc	cgg	aaa	ggc	771
Asp	Asp	Ile	Pro	Ala	Arg	Arg	Thr	Thr	Pro	Glu	Ala	Val	Arg	Lys	Gly	
		240				245						250				
cgc	acg	aac	gag	cga	ccg	gac	cgg	acg	tgg	gcg	acc	ggg	acg	acc	cca	819
Arg	Thr	Asn	Glu	Arg	Pro	Asp	Arg	Thr	Trp	Ala	Thr	Gly	Thr	Thr	Pro	
	255					260					265					
cgg	cca	cgg	cgt	tac	aag	gga	gag	acg	aag	gcc	aaa	aag	cac	cca	cgg	867
Arg	Pro	Arg	Arg	Tyr	Lys	Gly	Glu	Thr	Lys	Ala	Lys	Lys	His	Pro	Arg	
270					275					280					285	

ccg gaa tac aaa ggg acc tgg gtc acg ccg tta cag gac aac ccc act 915  
 Pro Glu Tyr Lys Gly Thr Trp Val Thr Pro Leu Gln Asp Asn Pro Thr  
 290 295 300

cca gcc ccc ccg aac gac cta tat cta ttc ttg gac ctg ggt gca gca 963  
 Pro Ala Pro Pro Asn Asp Leu Tyr Leu Phe Leu Asp Leu Gly Ala Ala  
 305 310 315

ggg aca cgg acc tgg acc gtg aaa tcg ggc tca atc acg aac aac atg 1011  
 Gly Thr Arg Thr Trp Thr Val Lys Ser Gly Ser Ile Thr Asn Asn Met  
 320 325 330

ata gtg aca acg tcc gtg gaa acc gcg acc gac ttc tca gag aaa acc 1059  
 Ile Val Thr Thr Ser Val Glu Thr Ala Thr Asp Phe Ser Glu Lys Thr  
 335 340 345

aag gtg gca aac acc acg acc gag ctc aac gac gga cgc gac gcc gga 1107  
 Lys Val Ala Asn Thr Thr Thr Glu Leu Asn Asp Gly Arg Asp Ala Gly  
 350 355 360 365

acg ggg atc ggt gcc gag cgc cac tgt gct gat gag aga tgg aaa gag 1155  
 Thr Gly Ile Gly Ala Glu Arg His Cys Ala Asp Glu Arg Trp Lys Glu  
 370 375 380

aca acg gta gcc ccc gat tgc gcc gta tcg gca gcg aac gcc tcg cga 1203  
 Thr Thr Val Ala Pro Asp Cys Ala Val Ser Ala Ala Asn Ala Ser Arg  
 385 390 395

cgc acc ggg gag ctg gcc acc ccg gtg acg atg ctg cct gat ccg ttg 1251  
 Arg Thr Gly Glu Leu Ala Thr Pro Val Thr Met Leu Pro Asp Pro Leu  
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tac gga ccg gaa taa aatcgacctga tgcct 1281  
 Tyr Gly Pro Glu  
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Pro Met Arg Trp Ala Trp Lys Arg Trp Gln Ala Val Gly Ala Ser Thr  
 35 40 45

Ala Arg Thr Trp Phe Gly Thr Glu Asn Gln Lys Gly Ile Thr Thr Ser  
 50 55 60

Thr Arg Ala Arg Arg Tyr Ala Val Ser Ala Lys Phe Pro Arg Leu Ser  
 65 70 75 80

Asn Lys Gly Lys Asp Tyr Met Arg Cys Val Leu Gln Tyr Thr Val Lys  
 85 90 95  
 Asn Glu Gln Lys Val Asp Cys Gly Gly Ser Tyr Ile Lys Leu Leu Pro  
 100 105 110  
 Ser Lys Leu Arg Thr Gly Asp Gly Asp Gly Val Ser Glu Tyr Ser Ile  
 115 120 125  
 Met Phe Gly Pro Asp Ser Thr Gly Ala Ser Arg Thr Val Arg Arg Ala  
 130 135 140  
 Arg Asn Tyr Lys Gly Lys Arg His Leu Arg Lys Lys Glu Gln Asn Lys  
 145 150 155 160  
 Val Glu Thr Asp Gln Leu Thr His Gln Tyr Thr Thr Ser Trp Ser Pro  
 165 170 175  
 Asp Trp Thr Tyr Asn Val Leu Val Asp Asn Lys Glu Ser Gln Ala Gly  
 180 185 190  
 Asn Leu Ala Asp Asp Cys Glu Leu Leu Pro Gln Lys Arg Ile Phe Arg  
 195 200 205  
 Pro Ser Cys Arg Lys Gln Ser Lys Pro Val Thr Cys Val Asp Val Lys  
 210 215 220  
 His His Ala Pro Arg Arg Asn Val Lys Pro Ala Gly His Asp Asp Ile  
 225 230 235 240  
 Pro Ala Arg Arg Thr Thr Pro Glu Ala Val Arg Lys Gly Arg Thr Asn  
 245 250 255  
 Glu Arg Pro Asp Arg Thr Trp Ala Thr Gly Thr Thr Pro Arg Pro Arg  
 260 265 270  
 Arg Tyr Lys Gly Glu Thr Lys Ala Lys Lys His Pro Arg Pro Glu Tyr  
 275 280 285  
 Lys Gly Thr Trp Val Thr Pro Leu Gln Asp Asn Pro Thr Pro Ala Pro  
 290 295 300  
 Pro Asn Asp Leu Tyr Leu Phe Leu Asp Leu Gly Ala Ala Gly Thr Arg  
 305 310 315 320  
 Thr Trp Thr Val Lys Ser Gly Ser Ile Thr Asn Asn Met Ile Val Thr  
 325 330 335  
 Thr Ser Val Glu Thr Ala Thr Asp Phe Ser Glu Lys Thr Lys Val Ala  
 340 345 350  
 Asn Thr Thr Thr Glu Leu Asn Asp Gly Arg Asp Ala Gly Thr Gly Ile  
 355 360 365  
 Gly Ala Glu Arg His Cys Ala Asp Glu Arg Trp Lys Glu Thr Thr Val  
 370 375 380



Ala Pro Asp Cys Ala Val Ser Ala Ala Asn Ala Ser Arg Arg Thr Gly  
385 390 395 400

Glu Leu Ala Thr Pro Val Thr Met Leu Pro Asp Pro Leu Tyr Gly Pro  
405 410 415

Glu

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<222> (1)..(411)

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aca aaa gag ctg gga aca gtt atg cgt tca cta gga caa aac cca aca 96  
Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr  
20 25 30  
gag gct gag ctc caa gac atg atc aac gag gtt gat gca gat gga aac 144  
Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn  
35 40 45  
ggc act atc gac ttc ccc gag ttc ctg aac ctg atg gct aag aag atg 192  
Gly Thr Ile Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Lys Lys Met  
50 55 60  
aaa gac act gac tcc gag gaa gag cta aaa gaa gcc ttc agg gtt ttc 240  
Lys Asp Thr Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe  
65 70 75 80  
gac aaa gac cag aac ggt ttc atc tcc gct gct gag cta cgc cat gtg 288  
Asp Lys Asp Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val  
85 90 95  
atg acc aat ctt ggt gag aag cta act gat gaa gaa gtg gaa gag atg 336  
Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Glu Glu Met  
100 105 110  
atc cgt gag gct gat gtt gat gga gat ggt cag att aac tat gaa gag 384  
Ile Arg Glu Ala Asp Val Asp Gly Asp Gly Gln Ile Asn Tyr Glu Glu  
115 120 125  
ttt gtc aag att atg atg gct aag tga tttgat 417  
Phe Val Lys Ile Met Met Ala Lys  
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 Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn  
 35 40 45  
 Gly Thr Ile Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Lys Lys Met  
 50 55 60  
 Lys Asp Thr Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe  
 65 70 75 80  
 Asp Lys Asp Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val  
 85 90 95  
 Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Glu Glu Met  
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 Phe Val Lys Ile Met Met Ala Lys  
 130 135

<210> 61  
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 <212> DNA  
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Ser	Asp	Arg	Ser	Thr	Pro	Pro	Ser	Leu	Asp	Glu	Arg	Ile	Asp	Leu	Val
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Leu	Phe	Ala	Gln	Ile	Ser	Lys	Gln	Thr	Arg	His	Asn	Pro	Asp	Arg	Gln
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Val	Ala	His	Asp	Ala	Thr	Ile	Glu	Pro	Asp	Ala	Gln	Val	Leu	Ala	Val
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Leu	Thr	Thr	Ile	Val	Phe	Phe	Leu	Asp	Glu	Thr	Phe	Glu	Glu	Ile	Ser
	290					295					300				
Tyr	Asp	Met	Ala	Thr	Thr	Val	Ser	Asp	Ala	Val	Glu	Leu	Ala	Gly	Thr
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Ile	Lys	Leu	Ser	Ala	Phe	Ser	Ser	Phe	Ser	Leu	Phe	Glu	Cys	Arg	Lys
				325						330				335	
Val	Val	Ser	Ser	Ser	Lys	Ser	Ser	Asp	Pro	Gly	Asn	Glu	Glu	Tyr	Ile



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Gly	Leu	Asp	Asp	Asn	Lys	Tyr	Ile	Gly	Asp	Leu	Leu	Ala	Glu	Phe	Lys
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Ala	Ile	Lys	Asp	Arg	Asn	Lys	Gly	Glu	Ile	Leu	His	Cys	Lys	Leu	Val
	370					375					380				
Phe	Lys	Lys	Lys	Leu	Phe	Arg	Glu	Ser	Asp	Glu	Ala	Val	Thr	Asp	Leu
385					390					395					400
Met	Phe	Val	Gln	Leu	Ser	Tyr	Val	Gln	Leu	Gln	His	Asp	Tyr	Leu	Leu
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Gly	Asn	Tyr	Pro	Val	Gly	Arg	Asp	Asp	Ala	Ala	Gln	Leu	Cys	Ala	Leu
			420					425					430		
Gln	Ile	Leu	Val	Gly	Ile	Gly	Phe	Val	Asn	Ser	Pro	Glu	Ser	Cys	Ile
	435					440						445			
Asp	Trp	Thr	Ser	Leu	Leu	Glu	Arg	Phe	Leu	Pro	Arg	Gln	Ile	Ala	Ile
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Thr	Arg	Ala	Lys	Arg	Glu	Trp	Glu	Leu	Asp	Ile	Leu	Ala	Arg	Tyr	Arg
465					470					475					480
Ser	Met	Glu	Asn	Val	Thr	Lys	Asp	Asp	Ala	Arg	Gln	Gln	Phe	Leu	Arg
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Ile	Leu	Lys	Ala	Leu	Pro	Tyr	Gly	Asn	Ser	Val	Phe	Phe	Ser	Val	Arg
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Ile	Asn	Lys	Arg	Gly	Val	His	Phe	Phe	Arg	Pro	Val	Pro	Lys	Glu	Tyr
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Leu	His	Ser	Ala	Glu	Leu	Arg	Asp	Ile	Met	Gln	Phe	Gly	Ser	Ser	Asn
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Thr	Ala	Val	Phe	Phe	Lys	Met	Arg	Val	Ala	Gly	Val	Leu	His	Ile	Phe
				565					570					575	
Gln	Phe	Glu	Thr	Lys	Gln	Gly	Glu	Glu	Ile	Cys	Val	Ala	Leu	Gln	Thr
			580				585						590		
His	Ile	Asn	Asp	Val	Met	Leu	Arg	Arg	Tyr	Ser	Lys	Ala	Arg	Ser	Ala
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Ala	Asn	Cys	Leu	Val	Asn	Gly	Asp	Ile	Ser	Cys	Cys	Ser	Lys	Pro	Gln
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Asn	Phe	Glu	Val	Tyr	Glu	Lys	Arg	Leu	Gln	Asp	Leu	Ser	Lys	Ala	Tyr
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Glu	Glu	Ser	Gln	Lys	Lys	Ile	Glu	Lys	Leu	Met	Asp	Glu	Gln	Gln	Glu

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Lys	Asn	Gln	Gln	Glu	Val	Thr	Leu	Arg	Glu	Glu	Leu	Glu	Ala	Ile	His				
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Asn	Gly	Leu	Glu	Leu	Glu	Arg	Arg	Lys	Leu	Leu	Glu	Val	Thr	Leu	Asp				
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Ser	Leu	Met	Ser	Glu	Leu	Arg	Gly	Met	Glu	Ala	Arg	Leu	Ala	Lys	Ser				
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Glu	Val	Glu	Ile	His	Gln	Lys	Arg	Tyr	Glu	Gln	Glu	Lys	Lys	Val	Leu				
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Leu	Leu	Leu	Gln	Asn	Asn	Leu	Lys	Glu	Leu	Glu	Glu	Leu	Arg	Glu	Met				
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Gln	Val	Leu	Arg	Lys	Arg	Tyr	Tyr	Asn	Thr	Ile	Glu	Asp	Met	Lys	Gly				
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Val	Phe	Asp	Met	Arg	Ala	Ser	Gln	Asp	Asp	Ile	Phe	Glu	Asp	Thr	Lys				

945	950	955	960
Tyr Leu Val Gln Ser Ala Val Asp Gly Tyr Asn Val Cys Ile Phe Ala	965	970	975
Tyr Gly Gln Thr Gly Ser Gly Lys Thr Phe Thr Ile Tyr Gly His Glu	980	985	990
Ser Asn Pro Gly Leu Thr Pro Arg Ala Thr Lys Glu Leu Phe Asn Ile	995	1000	1005
Leu Lys Arg Asp Ser Lys Arg Phe Ser Phe Ser Leu Lys Ala Tyr Met	1010	1015	1020
Val Glu Leu Tyr Gln Asp Thr Leu Val Asp Leu Leu Leu Pro Lys Ser	1025	1030	1035
Ala Arg Arg Leu Lys Leu Glu Ile Lys Lys Asp Ser Lys Gly Met Val	1045	1050	1055
Phe Val Glu Asn Val Thr Thr Ile Pro Ile Ser Thr Leu Glu Glu Leu	1060	1065	1070
Arg Met Ile Leu Glu Arg Gly Ser Glu Arg Arg His Val Ser Gly Thr	1075	1080	1085
Asn Met Asn Glu Glu Ser Ser Arg Ser His Leu Ile Leu Ser Val Val	1090	1095	1100
Ile Glu Ser Ile Asp Leu Gln Thr Gln Ser Ala Ala Arg Gly Lys Leu	1105	1110	1115
Ser Phe Val Asp Leu Ala Gly Ser Glu Arg Val Lys Lys Ser Gly Ser	1125	1130	1135
Ala Gly Cys Gln Leu Lys Glu Ala Gln Ser Ile Asn Lys Ser Leu Ser	1140	1145	1150
Ala Leu Gly Asp Val Ile Gly Ala Leu Ser Ser Gly Asn Gln His Ile	1155	1160	1165
Pro Tyr Arg Asn His Lys Leu Thr Met Leu Met Ser Asp Ser Leu Gly	1170	1175	1180
Gly Asn Ala Lys Thr Leu Met Phe Val Asn Val Ser Pro Ala Glu Ser	1185	1190	1195
Asn Leu Asp Glu Thr Tyr Asn Ser Leu Leu Tyr Ala Ser Arg Val Arg	1205	1210	1215
Thr Ile Val Asn Asp Pro Ser Lys His Ile Ser Ser Lys Glu Met Val	1220	1225	1230
Arg Leu Lys Lys Leu Val Ala Tyr Trp Lys Glu Gln Ala Gly Lys Lys	1235	1240	1245
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1250

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Val Pro Ile Asn Pro Pro Thr Thr Lys Arg Asp Leu Arg Gln Asn Asp	
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Asn Asn Asn Pro Lys Ser His Asn Ser His Asn Ser Asn Gly Met Thr	
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Lys Lys Ala Arg Ser Arg Leu Glu Thr His Pro Arg Asp Asn Glu Asn	
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Asn Tyr Arg Leu Ala Thr Ser Ala Gly Thr Lys Gly Gly Ala Arg Thr	
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gtt gac gta cca gtc ata tta agt acc cgg gaa tca caa ggc aca cgt	336
Val Asp Val Pro Val Ile Leu Ser Thr Arg Glu Ser Gln Gly Thr Arg	
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tca gta aat gca aca agt aaa att aga tgc ccg gat tcc act gca att	384
Ser Val Asn Ala Thr Ser Lys Ile Arg Cys Pro Asp Ser Thr Ala Ile	
115 120 125	
tgc gag tgg ttc gcc acg ccc acg gat cct caa aga cca gga gtt tat	432
Cys Glu Trp Phe Ala Thr Pro Thr Asp Pro Gln Arg Pro Gly Val Tyr	
130 135 140	
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Asn His Lys Asn Gly Asp Lys Asn Asn Arg Asp Thr Gly Asn Ile Asn	
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Thr Val Ser Ser Leu Met Asp Asn Ala Arg Gly Pro Asn Pro Arg Ser	
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Gly Ile Ser Ile Pro Thr Pro Thr Ser Arg Gln Ser Pro Ser Glu Thr	
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Pro Pro Asp Pro Leu Gln Asn Pro Asn Asn Tyr Thr Arg Tyr His Asn	
195 200 205	
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Asp Lys Asn Ser Lys Asn Ser Asn Arg Asn Tyr Asn Lys Arg Asn Lys	
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Asn Ser Thr Thr Phe Asn Asn Ser Asp Leu Pro Gly His Asn Arg Ser	
225 230 235 240	
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Ser Pro Ala Ile Asn Ala Val Lys Ser Ala Ser Asn Arg Ser Ser Ala	
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Ile Gly Ser Arg Asn Ser Asp Leu Asn Asn Ala Ala Asn Asp Glu Arg	
260 265 270	
cat tac gct aga tcg gga aca tat cag ata aac gct gta aca gta ctt	864
His Tyr Ala Arg Ser Gly Thr Tyr Gln Ile Asn Ala Val Thr Val Leu	
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Arg Val Leu Gly Arg Gly Ala Arg Arg Asp Val Lys Ser Ala Tyr His	
290 295 300	
ggc acc tgt ggt aca ggt ccc cgg atg aaa gtg ata aca ttg gct gtt	960
Gly Thr Cys Gly Thr Gly Pro Arg Met Lys Val Ile Thr Leu Ala Val	
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Gln Glu Asn Ile Arg Asn Arg Ile Ile Leu Glu Leu Arg Thr Leu His	
325 330 335	
aag acc tct tat caa tat atc gtt ccg tat tat gat ggg atc tat aca	1056
Lys Thr Ser Tyr Gln Tyr Ile Val Pro Tyr Tyr Asp Gly Ile Tyr Thr	
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Glu Gly Ser Ile Phe Ile Arg Met Val Glu Leu Gly Trp Val Thr Asn	
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atc atg aac aaa acg gcg acc ata cgt gcg ccg gtt ttg ggt acg atg	1152
Ile Met Asn Lys Thr Ala Thr Ile Arg Ala Pro Val Leu Gly Thr Met	
370 375 380	
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Ala Phe Leu Val Leu Gln Gly Arg Ile Tyr Val His Arg Lys Phe Asp 385 390 395 400	
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cta agc agt ggc gag tta ggt gaa agt cgt gag gtt gtg cca gac ggt Leu Ser Ser Gly Glu Leu Gly Glu Ser Arg Glu Val Val Pro Asp Gly 565 570 575	1728
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 Lys Lys Ala Arg Ser Arg Leu Glu Thr His Pro Arg Asp Asn Glu Asn  
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 Val Asp Val Pro Val Ile Leu Ser Thr Arg Glu Ser Gln Gly Thr Arg  
 100                      105                      110  
 Ser Val Asn Ala Thr Ser Lys Ile Arg Cys Pro Asp Ser Thr Ala Ile  
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 Cys Glu Trp Phe Ala Thr Pro Thr Asp Pro Gln Arg Pro Gly Val Tyr  
 130                      135                      140  
 Asn His Lys Asn Gly Asp Lys Asn Asn Arg Asp Thr Gly Asn Ile Asn  
 145                      150                      155                      160  
 Thr Val Ser Ser Leu Met Asp Asn Ala Arg Gly Pro Asn Pro Arg Ser  
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 Gly Ile Ser Ile Pro Thr Pro Thr Ser Arg Gln Ser Pro Ser Glu Thr

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Gln	Glu	Asn	Ile	Arg	Asn	Arg	Ile	Ile	Leu	Glu	Leu	Arg	Thr	Leu	His
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Lys	Thr	Ser	Tyr	Gln	Tyr	Ile	Val	Pro	Tyr	Tyr	Asp	Gly	Ile	Tyr	Thr
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Gln	His	Thr	Leu	Ser	Lys	Asp	Val	Thr	Ser	Val	Glu	Ser	Pro	Glu	Arg
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Tyr	Pro	Gln	Gln	Leu	Pro	Gln	Ala	Ser	Gln	His	Gln	Leu	Gln	Gln	Gln

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Ser Asn His Asp Ile Trp Asn Asn Arg Asn Arg Asp Lys Tyr Ile Ile		
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Ile Gly Leu Glu Val Leu Leu Asp Ser Ile Val Lys Glu Glu Val Arg		
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Met Glu Pro Ser Thr Val Ser Lys Glu Phe Arg Ser Ile Ile Ser Glu		
595	600	605
Cys Leu Arg Asn Asp Ala Thr Glu Arg Gln Thr Ala Ser Asn Leu Val		
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20	25
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Arg Lys Pro Pro Ser Asp Gly Phe Leu Lys Leu Pro Ala Ser Ser Ile	
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Ile	Ser	Ala	Val	Asn	Val	Ser	Ala	Gln	Ala	Ser	Leu	Thr	Ala	Asp	Phe	
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gac	aga	caa	caa	ctt	ctt	caa	caa	aag	ggt	tgt	gtc	gtt	tgg	atc	act	388
Asp	Arg	Gln	Gln	Leu	Leu	Gln	Gln	Lys	Gly	Cys	Val	Val	Trp	Ile	Thr	
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Ala	Leu	Phe	Glu	Arg	Gly	Lys	Leu	Thr	Tyr	Thr	Leu	Asp	Gly	Asp	Asn	
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Val	Gly	Val	Ile	Cys	Ile	Ala	Ser	Leu	Ile	Ser	Pro	Tyr	Arg	Arg	Asp	
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Arg	Asp	Ala	Cys	Arg	Ser	Leu	Leu	Pro	Asp	Gly	Asp	Phe	Val	Glu	Val	
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Phe	Met	Asp	Val	Pro	Leu	His	Val	Cys	Glu	Ser	Arg	Asp	Pro	Lys	Gly	
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Leu	Tyr	Lys	Leu	Ala	Arg	Ala	Gly	Lys	Ile	Lys	Gly	Phe	Thr	Gly	Ile	
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 Ser Leu Ile Ser Pro Tyr Arg Arg Asp Arg Asp Ala Cys Arg Ser Leu  
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 Leu Pro Asp Gly Asp Phe Val Glu Val Phe Met Asp Val Pro Leu His  
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Val Cys Glu Ser Arg Asp Pro Lys Gly Leu Tyr Lys Leu Ala Arg Ala  
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Gly Lys Ile Lys Gly Phe Thr Gly Ile Asp Asp Pro Tyr Glu Ala Pro  
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Val Asn Cys Glu Val Val Leu Lys His Thr Gly Asp Asp Glu Ser Cys  
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Ser Lys Ala Ser Ser Val Ser Val Arg Pro Ser Pro Arg Thr Glu Gly  
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Ala Ser Arg Pro Gly Thr Gly Leu Val Ile Ala Val Lys Lys Leu Asn  
95 100 105

caa gat ggt tgg caa ggt cac cag gag tgg ctg gct gaa gtg aat tac 387  
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Leu Glu Asp Glu His Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Gly	145	150	155	
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Ser Leu Glu Asn His Leu Phe Arg Arg Gly Leu Tyr Phe Gln Pro Leu	160	165	170	
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Ser Trp Lys Leu Arg Leu Lys Val Ala Leu Gly Ala Ala Lys Gly Leu	175	180	185	
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Phe Gly Leu Ala Lys Asp Gly Pro Ile Gly Asp Lys Ser His Val Ser	225	230	235	
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Thr Arg Val Met Gly Thr His Gly Tyr Ala Ala Pro Glu Tyr Leu Ala	240	245	250	
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Thr Gly His Leu Thr Thr Lys Ser Asp Val Tyr Ser Phe Gly Val Val	255	260	265	
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Leu Leu Glu Leu Leu Ser Gly Arg Arg Ala Val Asp Lys Asn Arg Pro	270	275	280	285
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Ser Gly Glu Arg Asn Leu Val Glu Trp Ala Lys Pro Tyr Leu Val Asn	290	295	300	
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Lys Arg Lys Ile Phe Arg Val Ile Asp Asn Arg Leu Gln Asp Gln Tyr	305	310	315	
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Ser Met Glu Glu Ala Cys Lys Val Ala Thr Leu Ser Leu Arg Cys Leu	320	325	330	
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Thr Thr Glu Ile Lys Leu Arg Pro Asn Met Ser Glu Val Val Ser His	335	340	345	

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Pro Gly Thr Gly Leu Val Ile Ala Val Lys Lys Leu Asn Gln Asp Gly  
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Phe Ser His Arg His Leu Val Lys Leu Ile Gly Tyr Cys Leu Glu Asp  
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Glu His Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Gly Ser Leu Glu  
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Ala	Gly	Phe	Ala	Arg	Gln	Thr	Ala	Val	Gly	Ser	Thr	Val	Val	Ala	Tyr				
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Val Arg Ile Cys  
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Ile Gly Lys Gly Ala Phe Gly Glu Val Arg Ile Cys Arg Glu Lys Gly
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Arg Phe Tyr Ile Gly Glu Thr Val Leu Ala Ile Glu Ser Ile His Lys
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Lys Asp Gly His Met Lys Leu Ser Asp Phe Gly Leu Cys Lys Pro Leu

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              1                      5

atg aac ggt gac gaa tgc gcg aac gtt gcg acg tgc tgg gtt act tct 102
Met Asn Gly Asp Glu Cys Ala Asn Val Ala Thr Cys Trp Val Thr Ser
 10                      15                      20                      25

cta gct tgt gta gtt gac gcc gga cga tat acg aaa aag gta tcc cac 150
Leu Ala Cys Val Val Asp Ala Gly Arg Tyr Thr Lys Lys Val Ser His
              30                      35                      40

gac cgg cga acg agg tgg ccc gcc tgg aaa gca cga cgg gat cgt cat 198
Asp Arg Arg Thr Arg Trp Pro Ala Trp Lys Ala Arg Arg Asp Arg His
              45                      50                      55

agt gtc cga agt gat agc ggc cta gac agt cat gca ctt gaa ggt gga 246
Ser Val Arg Ser Asp Ser Gly Leu Asp Ser His Ala Leu Glu Gly Gly
              60                      65                      70

aaa cga cgt gag tca tgc gta tca cta gct cac gaa cga gat tat gca 294
Lys Arg Arg Glu Ser Cys Val Ser Leu Ala His Glu Arg Asp Tyr Ala
              75                      80                      85

cta acg gca cgg tgg gat cgt agc att gca atg acg gat gac acg aac 342
Leu Thr Ala Arg Trp Asp Arg Ser Ile Ala Met Thr Asp Asp Thr Asn
 90                      95                      100                      105

cca caa acc caa cgt aaa ttt gag aaa cat act cgg gat gta gaa gct 390
Pro Gln Thr Gln Arg Lys Phe Glu Lys His Thr Arg Asp Val Glu Ala
              110                      115                      120

gtt cga ttt tct cca cga gat cgt cta att gta tct gcg ggt gca gat 438
Val Arg Phe Ser Pro Arg Asp Arg Leu Ile Val Ser Ala Gly Ala Asp
              125                      130                      135

ggg gta att gca gta tgt ccg gtt gct ggt gaa tgt gat gat gac gat 486
Gly Val Ile Ala Val Cys Pro Val Ala Gly Glu Cys Asp Asp Asp Asp
              140                      145                      150

gcc cgt gat ggt cat gaa gat tgt gtt agt agt att tgc ttt tca cca 534
Ala Arg Asp Gly His Glu Asp Cys Val Ser Ser Ile Cys Phe Ser Pro
              155                      160                      165

tca cta gaa cac ccg atc ctc ttt tct ggt agt tgt atc tac ttt att 582
Ser Leu Glu His Pro Ile Leu Phe Ser Gly Ser Cys Ile Tyr Phe Ile

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[illegible]

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<210> 72
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<213> Arabidopsis thaliana
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Asn Val Ala Thr Cys Trp Val Thr Ser Leu Ala Cys Val Val Asp Ala
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Gly Arg Tyr Thr Lys Lys Val Ser His Asp Arg Arg Thr Arg Trp Pro
          35                                40                        45
Ala Trp Lys Ala Arg Arg Asp Arg His Ser Val Arg Ser Asp Ser Gly
      50                                  55                  60
Leu Asp Ser His Ala Leu Glu Gly Gly Lys Arg Arg Glu Ser Cys Val
   65                             70                         75           80
Ser Leu Ala His Glu Arg Asp Tyr Ala Leu Thr Ala Arg Trp Asp Arg
                    85                              90              95
Ser Ile Ala Met Thr Asp Asp Thr Asn Pro Gln Thr Gln Arg Lys Phe
    100                                   105                   110
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Glu Lys His Thr Arg Asp Val Glu Ala Val Arg Phe Ser Pro Arg Asp  
 115 120 125  
 Arg Leu Ile Val Ser Ala Gly Ala Asp Gly Val Ile Ala Val Cys Pro  
 130 135 140  
 Val Ala Gly Glu Cys Asp Asp Asp Asp Ala Arg Asp Gly His Glu Asp  
 145 150 155 160  
 Cys Val Ser Ser Ile Cys Phe Ser Pro Ser Leu Glu His Pro Ile Leu  
 165 170 175  
 Phe Ser Gly Ser Cys Ile Tyr Phe Ile Lys Val Trp Asn Val Asn Gly  
 180 185 190  
 Lys Lys Cys Arg Thr Pro Leu Lys Lys His Ser Asn Pro Val Ser Thr  
 195 200 205  
 Arg Thr Gln Ser Glu Glu Gly Arg Leu Cys Ala Lys Gly Gly Lys Ser  
 210 215 220  
 Gly Ala Arg Leu Leu Pro Asp Leu Ser Thr Gln Glu Gln Leu Pro Lys  
 225 230 235 240  
 Ile Asn Gln Glu Asn Pro Ile Asn Gln Ile Ala Phe Ser Pro Ser Pro  
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 260 265 270

<210> 73  
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<220>  
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 <222> (750)..(1193)

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 Met Lys Arg Leu Ser  
 1 5



agc tca gat tca atg tgt ggt cta atc tcc act tct aca g gttcttatta 165  
 Ser Ser Asp Ser Met Cys Gly Leu Ile Ser Thr Ser Thr A  
 10 15

ccattcttgt tctttctact ttttgcta at gtcagacaaa acccatgtga tcctttcttc 225  
 actttccact gtttctttta ttgacaag at tca ttt ggt tac aca aca gat gaa 279  
 sp Ser Phe Gly Tyr Thr Thr Asp Glu  
 20 25

cag agt cca aga ggg tac gga agt aat tac caa tct atg ctt gaa ggt 327  
 Gln Ser Pro Arg Gly Tyr Gly Ser Asn Tyr Gln Ser Met Leu Glu Gly  
 30 35 40

tac gat gaa gat gct aca cta atc gag gaa tat tcc ggc aac cac cac 375  
 Tyr Asp Glu Asp Ala Thr Leu Ile Glu Glu Tyr Ser Gly Asn His His  
 45 50 55

cac atg ggt cta tcg gag aag aag aga aga tta aaa gtt gac caa gtc 423  
 His Met Gly Leu Ser Glu Lys Lys Arg Arg Leu Lys Val Asp Gln Val  
 60 65 70 75

aaa gct ctt gag aag aat ttc gaa ctt gag aat aaa ctc gaa cct gag 471  
 Lys Ala Leu Glu Lys Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu  
 80 85 90

agg aaa act aaa tta gca caa gag ctt gga ctt caa cct cgt caa gta 519  
 Arg Lys Thr Lys Leu Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val  
 95 100 105

gct gtt tgg ttt cag aac cgt cgt gca cgg tgg aaa aca aaa cag ctt 567  
 Ala Val Trp Phe Gln Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu  
 110 115 120

gaa aaa gat tac ggt gtt ctt aag ggt caa tac gat tct ctc cgc cac 615  
 Glu Lys Asp Tyr Gly Val Leu Lys Gly Gln Tyr Asp Ser Leu Arg His  
 125 130 135

aat ttc gat tct ctc cgc cgt gac aat gat tcc ctt ctc caa gag 660  
 Asn Phe Asp Ser Leu Arg Arg Asp Asn Asp Ser Leu Leu Gln Glu  
 140 145 150

gtacaatatt agagacttta aaccataaaa attgaaactt cagagacgaa aatgcaaaaa 720

gggttgatatt ttaaagtttt tggttgacag att agt aaa atc aaa gct aag gta 773  
 Ile Ser Lys Ile Lys Ala Lys Val  
 155 160

aac ggt gaa gaa gat aac aac aac aac aaa gct att acg gag ggt gtt 821  
 Asn Gly Glu Glu Asp Asn Asn Asn Asn Lys Ala Ile Thr Glu Gly Val  
 165 170 175

aag gaa gag gaa gtt cac aag acg gat tcg att cct tcg tct cct ctg 869  
 Lys Glu Glu Glu Val His Lys Thr Asp Ser Ile Pro Ser Ser Pro Leu  
 180 185 190

cag ttt cta gaa cat tcc tct ggt ttt aac tac cgg cga agc ttc act 917

Gln Phe Leu Glu His Ser Ser Gly Phe Asn Tyr Arg Arg Ser Phe Thr  
 195 200 205 210  
 gac ctc cgt gac ctt cta ccg aat tcc acc gtt gtc gag gct gga tct 965  
 Asp Leu Arg Asp Leu Leu Pro Asn Ser Thr Val Val Glu Ala Gly Ser  
 215 220 225  
 tcc gat agt tgc gat tca agc gcc gtt ctt aac gac gaa aca agt tct 1013  
 Ser Asp Ser Cys Asp Ser Ser Ala Val Leu Asn Asp Glu Thr Ser Ser  
 230 235 240  
 gat aac gga aga ttg acg ccg cct gtg acg gtt act ggc ggg agt ttc 1061  
 Asp Asn Gly Arg Leu Thr Pro Pro Val Thr Val Thr Gly Gly Ser Phe  
 245 250 255  
 tta cag ttt gtg aaa aca gag caa aca gag gat cac gag gat ttt cta 1109  
 Leu Gln Phe Val Lys Thr Glu Gln Thr Glu Asp His Glu Asp Phe Leu  
 260 265 270  
 agc ggt gaa gaa gct tgt ggt ttc ttc tcc gat gaa cag ccg ccg tca 1157  
 Ser Gly Glu Glu Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro Pro Ser  
 275 280 285 290  
 ctt cat tgg tac tct gct tca gat cat tgg act tga gaattgttta 1203  
 Leu His Trp Tyr Ser Ala Ser Asp His Trp Thr  
 295 300  
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&lt;210&gt; 74

&lt;211&gt; 301

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 74

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 20 25 30  
 Tyr Gly Ser Asn Tyr Gln Ser Met Leu Glu Gly Tyr Asp Glu Asp Ala  
 35 40 45  
 Thr Leu Ile Glu Glu Tyr Ser Gly Asn His His His Met Gly Leu Ser  
 50 55 60  
 Glu Lys Lys Arg Arg Leu Lys Val Asp Gln Val Lys Ala Leu Glu Lys  
 65 70 75 80  
 Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu Arg Lys Thr Lys Leu  
 85 90 95  
 Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val Ala Val Trp Phe Gln  
 100 105 110

Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu Glu Lys Asp Tyr Gly  
 115 120 125  
 Val Leu Lys Gly Gln Tyr Asp Ser Leu Arg His Asn Phe Asp Ser Leu  
 130 135 140  
 Arg Arg Asp Asn Asp Ser Leu Leu Gln Glu Ile Ser Lys Ile Lys Ala  
 145 150 155 160  
 Lys Val Asn Gly Glu Glu Asp Asn Asn Asn Asn Lys Ala Ile Thr Glu  
 165 170 175  
 Gly Val Lys Glu Glu Glu Val His Lys Thr Asp Ser Ile Pro Ser Ser  
 180 185 190  
 Pro Leu Gln Phe Leu Glu His Ser Ser Gly Phe Asn Tyr Arg Arg Ser  
 195 200 205  
 Phe Thr Asp Leu Arg Asp Leu Leu Pro Asn Ser Thr Val Val Glu Ala  
 210 215 220  
 Gly Ser Ser Asp Ser Cys Asp Ser Ser Ala Val Leu Asn Asp Glu Thr  
 225 230 235 240  
 Ser Ser Asp Asn Gly Arg Leu Thr Pro Pro Val Thr Val Thr Gly Gly  
 245 250 255  
 Ser Phe Leu Gln Phe Val Lys Thr Glu Gln Thr Glu Asp His Glu Asp  
 260 265 270  
 Phe Leu Ser Gly Glu Glu Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro  
 275 280 285  
 Pro Ser Leu His Trp Tyr Ser Ala Ser Asp His Trp Thr  
 290 295 300

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 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> CDS  
 <222> (22)..(1122)

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 agc tcg atc cgt tgg ttt gcc aac cga tta gtg agt ggt agc ctg tta 99  
 Ser Ser Ile Arg Trp Phe Ala Asn Arg Leu Val Ser Gly Ser Leu Leu  
 15 20 25  
 ttg tgt gct aac gcc tac agt cgt cgt act ccc gcg tcc ggg gcc gca 147

Leu	Cys	Ala	Asn	Ala	Tyr	Ser	Arg	Arg	Thr	Pro	Ala	Ser	Gly	Ala	Ala		
			30					35					40				
tta	cag	cag	atg	aac	cgt	gcc	agt	cag	tca	gtg	aat	tac	cga	cga	cgt	195	
Leu	Gln	Gln	Met	Asn	Arg	Ala	Ser	Gln	Ser	Val	Asn	Tyr	Arg	Arg	Arg		
		45					50				55						
gag	ctg	tca	tta	atc	agc	ggc	cgg	aaa	cag	ggg	gtc	cag	tct	ctg	ggg	243	
Glu	Leu	Ser	Leu	Ile	Ser	Gly	Arg	Lys	Gln	Gly	Val	Gln	Ser	Leu	Gly		
	60					65				70							
tat	aga	ctt	gca	cgc	ctc	gat	aac	cgc	gct	ctt	gca	caa	ttg	ttg	cac	291	
Tyr	Arg	Leu	Ala	Arg	Leu	Asp	Asn	Arg	Ala	Leu	Ala	Gln	Leu	Leu	His		
	75				80				85						90		
agg	gat	ggc	cag	ccc	gag	gaa	gtg	gta	cag	cgc	ggc	aat	gaa	atc	agc	339	
Arg	Asp	Gly	Gln	Pro	Glu	Glu	Val	Val	Gln	Arg	Gly	Asn	Glu	Ile	Ser		
				95					100					105			
tat	ttc	gaa	acg	gga	ctt	gaa	ccg	acc	acg	ctt	aga	cgt	gtg	cgc	gat	387	
Tyr	Phe	Glu	Thr	Gly	Leu	Glu	Pro	Thr	Thr	Leu	Arg	Arg	Val	Arg	Asp		
			110					115					120				
tgt	gtt	gtt	gcc	gct	ctg	cca	acc	gtt	atc	tat	acc	gga	ttc	aaa	cgt	435	
Cys	Val	Val	Ala	Ala	Leu	Pro	Thr	Val	Ile	Tyr	Thr	Gly	Phe	Lys	Arg		
		125					130					135					
gtt	tct	cct	tac	tac	gaa	ttt	atc	tcc	gtc	ggg	cgc	acg	agg	gtt	gct	483	
Val	Ser	Pro	Tyr	Tyr	Glu	Phe	Ile	Ser	Val	Gly	Arg	Thr	Arg	Val	Ala		
	140					145					150						
gat	cgt	ctt	agc	gaa	gtc	acg	caa	gtg	gtt	ccc	cga	gat	gat	aca	cgc	531	
Asp	Arg	Leu	Ser	Glu	Val	Thr	Gln	Val	Val	Pro	Arg	Asp	Asp	Thr	Arg		
	155				160					165					170		
tac	gtc	tac	atc	gtg	tgg	cgg	gaa	tcc	gaa	cga	tcg	aaa	tta	gag	gcg	579	
Tyr	Val	Tyr	Ile	Val	Trp	Arg	Glu	Ser	Glu	Arg	Ser	Lys	Leu	Glu	Ala		
			175					180						185			
cgg	ggg	gat	ctc	cgt	gat	cgc	gat	ggg	gaa	acg	ctg	gaa	aag	ttt	cgc	627	
Arg	Gly	Asp	Leu	Arg	Asp	Arg	Asp	Gly	Glu	Thr	Leu	Glu	Lys	Phe	Arg		
			190					195					200				
gtg	att	gct	ttt	aac	gtc	acg	ctg	gat	atc	agc	agc	agt	atg	gag	ccg	675	
Val	Ile	Ala	Phe	Asn	Val	Thr	Leu	Asp	Ile	Ser	Ser	Ser	Met	Glu	Pro		
		205					210					215					
ctg	gcg	aag	gga	gat	ttg	ccg	ccg	ttg	ctt	gct	gtt	cct	gta	ggg	gaa	723	
Leu	Ala	Lys	Gly	Asp	Leu	Pro	Pro	Leu	Leu	Ala	Val	Pro	Val	Gly	Glu		
	220					225					230						
caa	gct	aga	ttc	agc	ttg	acg	cca	acc	tgg	ttg	cca	cag	ggg	cgt	agc	771	
Gln	Ala	Arg	Phe	Ser	Leu	Thr	Pro	Thr	Trp	Leu	Pro	Gln	Gly	Arg	Ser		
	235				240				245					250			
gat	gtt	tcc	agt	agt	cga	cgt	ggg	cta	ccg	cgg	atg	gac	aaa	gtg	cct	819	
Asp	Val	Ser	Ser	Ser	Arg	Arg	Gly	Leu	Pro	Arg	Met	Asp	Lys	Val	Pro		

255										260					265					
atc	gaa	tcc	cgt	ctc	tcg	acc	gac	gga	gta	ttc	agc	ttc	tcg	gta	aac	867				
Ile	Glu	Ser	Arg	Leu	Ser	Thr	Asp	Gly	Val	Phe	Ser	Phe	Ser	Val	Asn					
			270					275					280							
gtt	aac	ggc	gct	acg	cca	tcg	agg	tgg	gat	cag	atg	ttg	cgc	acc	gga	915				
Val	Asn	Gly	Ala	Thr	Pro	Ser	Arg	Trp	Asp	Gln	Met	Leu	Arg	Thr	Gly					
		285					290					295								
cgc	agg	ccc	gtc	agt	aga	agc	gta	cgt	gat	gtc	gcc	gaa	aac	acc	att	963				
Arg	Arg	Pro	Val	Ser	Arg	Ser	Val	Arg	Asp	Val	Ala	Glu	Asn	Thr	Ile					
		300				305					310									
ggc	ggt	gaa	ctg	ccg	ccg	cgt	agc	tgc	tcg	cga	ccc	gat	ccg	ttg	acc	1011				
Gly	Gly	Glu	Leu	Pro	Pro	Arg	Ser	Cys	Ser	Arg	Pro	Asp	Pro	Leu	Thr					
315					320					325					330					
gct	gac	cgc	cga	cgc	tgc	gct	agc	ctg	agc	ctg	ccc	agc	ctg	cca	gct	1059				
Ala	Asp	Arg	Arg	Arg	Cys	Ala	Ser	Leu	Ser	Leu	Pro	Ser	Leu	Pro	Ala					
				335				340						345						
cga	cag	ccc	tcc	caa	acg	gag	aaa	cgc	att	gtc	gag	aat	att	aag	tac	1107				
Arg	Gln	Pro	Ser	Gln	Thr	Glu	Lys	Arg	Ile	Val	Glu	Asn	Ile	Lys	Tyr					
			350					355					360							
ggg	gca	gcg	cca	tga												1122				
Gly	Ala	Ala	Pro																	
			365																	

&lt;210&gt; 76

&lt;211&gt; 366

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 76

Met	Asn	Gln	Arg	Ala	Asp	Arg	Asp	Arg	Ala	Ser	Ser	Ile	Arg	Trp	Phe
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Ala	Asn	Arg	Leu	Val	Ser	Gly	Ser	Leu	Leu	Leu	Cys	Ala	Asn	Ala	Tyr
			20					25					30		

Ser	Arg	Arg	Thr	Pro	Ala	Ser	Gly	Ala	Ala	Leu	Gln	Gln	Met	Asn	Arg
			35				40					45			

Ala	Ser	Gln	Ser	Val	Asn	Tyr	Arg	Arg	Arg	Glu	Leu	Ser	Leu	Ile	Ser
		50				55					60				

Gly	Arg	Lys	Gln	Gly	Val	Gln	Ser	Leu	Gly	Tyr	Arg	Leu	Ala	Arg	Leu
65				70					75					80	

Asp	Asn	Arg	Ala	Leu	Ala	Gln	Leu	Leu	His	Arg	Asp	Gly	Gln	Pro	Glu
			85						90					95	

Glu	Val	Val	Gln	Arg	Gly	Asn	Glu	Ile	Ser	Tyr	Phe	Glu	Thr	Gly	Leu
			100					105						110	

Glu Pro Thr Thr Leu Arg Arg Val Arg Asp Cys Val Val Ala Ala Leu  
 115 120 125  
 Pro Thr Val Ile Tyr Thr Gly Phe Lys Arg Val Ser Pro Tyr Tyr Glu  
 130 135 140  
 Phe Ile Ser Val Gly Arg Thr Arg Val Ala Asp Arg Leu Ser Glu Val  
 145 150 155 160  
 Thr Gln Val Val Pro Arg Asp Asp Thr Arg Tyr Val Tyr Ile Val Trp  
 165 170 175  
 Arg Glu Ser Glu Arg Ser Lys Leu Glu Ala Arg Gly Asp Leu Arg Asp  
 180 185 190  
 Arg Asp Gly Glu Thr Leu Glu Lys Phe Arg Val Ile Ala Phe Asn Val  
 195 200 205  
 Thr Leu Asp Ile Ser Ser Ser Met Glu Pro Leu Ala Lys Gly Asp Leu  
 210 215 220  
 Pro Pro Leu Leu Ala Val Pro Val Gly Glu Gln Ala Arg Phe Ser Leu  
 225 230 235 240  
 Thr Pro Thr Trp Leu Pro Gln Gly Arg Ser Asp Val Ser Ser Ser Arg  
 245 250 255  
 Arg Gly Leu Pro Arg Met Asp Lys Val Pro Ile Glu Ser Arg Leu Ser  
 260 265 270  
 Thr Asp Gly Val Phe Ser Phe Ser Val Asn Val Asn Gly Ala Thr Pro  
 275 280 285  
 Ser Arg Trp Asp Gln Met Leu Arg Thr Gly Arg Arg Pro Val Ser Arg  
 290 295 300  
 Ser Val Arg Asp Val Ala Glu Asn Thr Ile Gly Gly Glu Leu Pro Pro  
 305 310 315 320  
 Arg Ser Cys Ser Arg Pro Asp Pro Leu Thr Ala Asp Arg Arg Arg Cys  
 325 330 335  
 Ala Ser Leu Ser Leu Pro Ser Leu Pro Ala Arg Gln Pro Ser Gln Thr  
 340 345 350  
 Glu Lys Arg Ile Val Glu Asn Ile Lys Tyr Gly Ala Ala Pro  
 355 360 365

&lt;210&gt; 77

&lt;211&gt; 1650

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;



<221> CDS  
<222> (21)..(203)

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<222> (291)..(482)

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<222> (633)..(838)

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<400> 77

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Leu Glu Gly Asp Phe Asn Lys Asp Asn Thr Ser Ser Ala Thr Glu Ile  
15 20 25

gat act tta gag aac tta gat gac act agg cag ata agt aaa gga aaa 149  
Asp Thr Leu Glu Asn Leu Asp Asp Thr Arg Gln Ile Ser Lys Gly Lys  
30 35 40

cct ccg agg cac ctc aca agc agt gct act agg ctg cag ctt gca gcc 197  
Pro Pro Arg His Leu Thr Ser Ser Ala Thr Arg Leu Gln Leu Ala Ala  
45 50 55

aat gcg gtaatatct tgaccctgct ttttcttttt ccttttcttt gttacaatgg 253  
Asn Ala  
60

gattcgaatg atgtaactgg tttctgtttg tgcgcag gat gtg gat gtt tgt aac 308  
Asp Val Asp Val Cys Asn  
65

ttg gtt atg aag tca ctt gat gac aaa tca gag ttt cta cct gta tac 356  
Leu Val Met Lys Ser Leu Asp Asp Lys Ser Glu Phe Leu Pro Val Tyr  
70 75 80

cga tca gga agt tgt gct gag caa ggg gca aaa cag ttc atg gaa gat 404  
Arg Ser Gly Ser Cys Ala Glu Gln Gly Ala Lys Gln Phe Met Glu Asp  
85 90 95

gaa cac att tgc atc gat gat ctt gtt aat cat ctt ggt gca gct att 452  
Glu His Ile Cys Ile Asp Asp Leu Val Asn His Leu Gly Ala Ala Ile  
100 105 110 115

caa tgc tct tct ctt gga gcc ttc tat ggg gtgagtttat cttccaatct 502  
Gln Cys Ser Ser Leu Gly Ala Phe Tyr Gly  
120 125

tacccaaaga agcataaaaag caattcacta gcctgattct tctttcttct cctcttttgt 562

actagtagca tataagaggt attacttcaa aaactcttct aacatttggt gattgtgtgt 622

cctttggcag gta ttt gat ggc cac ggt ggc aca gat gca gca cac ttt 671  
 Val Phe Asp Gly His Gly Gly Thr Asp Ala Ala His Phe  
 130 135

ggt aga aag aac att ctg aga ttc att gta gag gac tcc tcc ttc cca 719  
 Val Arg Lys Asn Ile Leu Arg Phe Ile Val Glu Asp Ser Ser Phe Pro  
 140 145 150

cta tgc gta aag aaa gca att aag agt gct ttc tta aaa gct gat tat 767  
 Leu Cys Val Lys Lys Ala Ile Lys Ser Ala Phe Leu Lys Ala Asp Tyr  
 155 160 165 170

gaa ttt gca gat gat tct tct ctt gac atc tct tct ggg acc act gcg 815  
 Glu Phe Ala Asp Asp Ser Ser Leu Asp Ile Ser Ser Gly Thr Thr Ala  
 175 180 185

ctt aca gct ttt att ttt gga cg gtaagagcat ttaaattcgt atttatgaac 868  
 Leu Thr Ala Phe Ile Phe Gly Ar  
 190

ttgggaagct atatatgtta tcacctgtat aatcatcaat acttatcagg ttgcctgtgt 928

gtataagata gagaataagg cttagtgtaa agacttatgt aacgggctgt tttaccatgt 988

ttctttgtag ttttgatgtg attttgaata gaattgctac tttctttctt tacag g 1044  
 g

agg ttg ata att gca aat gct ggt gat tgc cga gca gta ctg ggg aga 1092  
 Arg Leu Ile Ile Ala Asn Ala Gly Asp Cys Arg Ala Val Leu Gly Arg  
 195 200 205 210

aga ggt agg gca att gag ttg tcc aaa gat cac aaa cca aac tgc aca 1140  
 Arg Gly Arg Ala Ile Glu Leu Ser Lys Asp His Lys Pro Asn Cys Thr  
 215 220 225

gcc gag aaa gta aga ata gaa aag tta ggt gga gtt gtg tat gac ggt 1188  
 Ala Glu Lys Val Arg Ile Glu Lys Leu Gly Gly Val Val Tyr Asp Gly  
 230 235 240

tac ctc aac ggg caa cta tca gtt gca cgt gcc att gga gac tgg cac 1236  
 Tyr Leu Asn Gly Gln Leu Ser Val Ala Arg Ala Ile Gly Asp Trp His  
 245 250 255

atg aaa ggt ccc aaa ggc tct gct tgt ccg cta agc cca gag cca gag 1284  
 Met Lys Gly Pro Lys Gly Ser Ala Cys Pro Leu Ser Pro Glu Pro Glu  
 260 265 270

ttg caa gag aca gac ctg agt gaa gac gac gag ttc ttg ata atg gga 1332  
 Leu Gln Glu Thr Asp Leu Ser Glu Asp Asp Glu Phe Leu Ile Met Gly  
 275 280 285 290

tgt gat ggt ctg tgg gat gtg atg agc agc cag tgc gct gtg aca ata 1380  
 Cys Asp Gly Leu Trp Asp Val Met Ser Ser Gln Cys Ala Val Thr Ile  
 295 300 305

gct agg aag gaa ctg atg att cat aat gat cca gag aga tgc tct aga 1428  
 Ala Arg Lys Glu Leu Met Ile His Asn Asp Pro Glu Arg Cys Ser Arg  
                   310                                  315                                  320

gag ctt gtg agg gag gcc ctt aaa cgg aat aca tgt gac aat ttg aca 1476  
 Glu Leu Val Arg Glu Ala Leu Lys Arg Asn Thr Cys Asp Asn Leu Thr  
                   325                                  330                                  335

gtg att gtt gtg tgc ttc tct ccg gat cct cca cag agg ata gag atc 1524  
 Val Ile Val Val Cys Phe Ser Pro Asp Pro Pro Gln Arg Ile Glu Ile  
                   340                                  345                                  350

cga atg cag tca cgg gtg agg cgg agc ata tct gcg gaa ggg tta aac 1572  
 Arg Met Gln Ser Arg Val Arg Arg Ser Ile Ser Ala Glu Gly Leu Asn  
                   355                                  360                                  365                                  370

cta ctc aaa ggc gtg ctc gat ggc tat ccg tga gcatgttatg ttgtacgtta 1625  
 Leu Leu Lys Gly Val Leu Asp Gly Tyr Pro  
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ctttgtgaga ctattgccaa gtttag 1650

<210> 78

<211> 380

<212> PRT

<213> Arabidopsis thaliana

<400> 78

Met Ser Met Asp Phe Ser Pro Leu Leu Thr Val Leu Glu Gly Asp Phe  
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Asn Lys Asp Asn Thr Ser Ser Ala Thr Glu Ile Asp Thr Leu Glu Asn  
                   20                                  25                                  30

Leu Asp Asp Thr Arg Gln Ile Ser Lys Gly Lys Pro Pro Arg His Leu  
                   35                                  40                                  45

Thr Ser Ser Ala Thr Arg Leu Gln Leu Ala Ala Asn Ala Asp Val Asp  
           50                                  55                                  60

Val Cys Asn Leu Val Met Lys Ser Leu Asp Asp Lys Ser Glu Phe Leu  
           65                                  70                                  75                                  80

Pro Val Tyr Arg Ser Gly Ser Cys Ala Glu Gln Gly Ala Lys Gln Phe  
                   85                                  90                                  95

Met Glu Asp Glu His Ile Cys Ile Asp Asp Leu Val Asn His Leu Gly  
                   100                                  105                                  110

Ala Ala Ile Gln Cys Ser Ser Leu Gly Ala Phe Tyr Gly Val Phe Asp  
           115                                  120                                  125

Gly His Gly Gly Thr Asp Ala Ala His Phe Val Arg Lys Asn Ile Leu  
           130                                  135                                  140

Arg Phe Ile Val Glu Asp Ser Ser Phe Pro Leu Cys Val Lys Lys Ala  
 145 150 155 160  
 Ile Lys Ser Ala Phe Leu Lys Ala Asp Tyr Glu Phe Ala Asp Asp Ser  
 165 170 175  
 Ser Leu Asp Ile Ser Ser Gly Thr Thr Ala Leu Thr Ala Phe Ile Phe  
 180 185 190  
 Gly Arg Arg Leu Ile Ile Ala Asn Ala Gly Asp Cys Arg Ala Val Leu  
 195 200 205  
 Gly Arg Arg Gly Arg Ala Ile Glu Leu Ser Lys Asp His Lys Pro Asn  
 210 215 220  
 Cys Thr Ala Glu Lys Val Arg Ile Glu Lys Leu Gly Gly Val Val Tyr  
 225 230 235 240  
 Asp Gly Tyr Leu Asn Gly Gln Leu Ser Val Ala Arg Ala Ile Gly Asp  
 245 250 255  
 Trp His Met Lys Gly Pro Lys Gly Ser Ala Cys Pro Leu Ser Pro Glu  
 260 265 270  
 Pro Glu Leu Gln Glu Thr Asp Leu Ser Glu Asp Asp Glu Phe Leu Ile  
 275 280 285  
 Met Gly Cys Asp Gly Leu Trp Asp Val Met Ser Ser Gln Cys Ala Val  
 290 295 300  
 Thr Ile Ala Arg Lys Glu Leu Met Ile His Asn Asp Pro Glu Arg Cys  
 305 310 315 320  
 Ser Arg Glu Leu Val Arg Glu Ala Leu Lys Arg Asn Thr Cys Asp Asn  
 325 330 335  
 Leu Thr Val Ile Val Val Cys Phe Ser Pro Asp Pro Pro Gln Arg Ile  
 340 345 350  
 Glu Ile Arg Met Gln Ser Arg Val Arg Arg Ser Ile Ser Ala Glu Gly  
 355 360 365  
 Leu Asn Leu Leu Lys Gly Val Leu Asp Gly Tyr Pro  
 370 375 380

<210> 79  
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<220>  
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<400> 79

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              1              5              10

gag gtg cca aag gta gca aca gag gaa tca tcg gca gag gtt aca gat      98
Glu Val Pro Lys Val Ala Thr Glu Glu Ser Ser Ala Glu Val Thr Asp
              15              20              25

cgt gga ttg ttc gat ttc ttg gga aag aag aaa gac gaa aca aaa cca      146
Arg Gly Leu Phe Asp Phe Leu Gly Lys Lys Lys Asp Glu Thr Lys Pro
              30              35              40

gag gag act ccg atc gct tca gag ttt gag cag aag gtt cat att tca      194
Glu Glu Thr Pro Ile Ala Ser Glu Phe Glu Gln Lys Val His Ile Ser
              45              50              55

gag ccg gag cca gag gtt aaa cac gaa agt ctt ctt gaa aag ctt cac      242
Glu Pro Glu Pro Glu Val Lys His Glu Ser Leu Leu Glu Lys Leu His
              60              65              70              75

cga agc gac agt tct tct agc tcc tca agt gag gaa gaa ggt tca gat      290
Arg Ser Asp Ser Ser Ser Ser Ser Ser Ser Glu Glu Glu Gly Ser Asp
              80              85              90

ggt gag aag agg aag aag aag aag gag aag aag aag cca act act gaa      338
Gly Glu Lys Arg Lys Lys Lys Lys Glu Lys Lys Lys Pro Thr Thr Glu
              95              100              105

gtt gag gta aag gag gaa gag aag aaa ggg ttt atg gag aag ttg aaa      386
Val Glu Val Lys Glu Glu Glu Lys Lys Gly Phe Met Glu Lys Leu Lys
              110              115              120

gag aag ctt cct gga cac aag aaa cct gaa gac ggt tca gcc gtc gct      434
Glu Lys Leu Pro Gly His Lys Lys Pro Glu Asp Gly Ser Ala Val Ala
              125              130              135

gcg gca ccg gtg gtt gtt cct cct cct gtg gaa gaa gcg cat cca gtg      482
Ala Ala Pro Val Val Val Pro Pro Pro Val Glu Glu Ala His Pro Val
              140              145              150              155

gag aag aaa ggg att ctt gag aag att aag gag aag ctt cca gga tac      530
Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Glu Lys Leu Pro Gly Tyr
              160              165              170

cac cct aag acc acc gta gag gag gag aag aaa gat aaa gaa taa      575
His Pro Lys Thr Thr Val Glu Glu Glu Lys Lys Asp Lys Glu
              175              180              185

gaagattatc attaa      590

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&lt;210&gt; 80

&lt;211&gt; 185

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 80

Met Ala Glu Glu Ile Lys Asn Val Pro Glu Gln Glu Val Pro Lys Val  
 1 5 10 15  
 Ala Thr Glu Glu Ser Ser Ala Glu Val Thr Asp Arg Gly Leu Phe Asp  
 20 25 30  
 Phe Leu Gly Lys Lys Lys Asp Glu Thr Lys Pro Glu Glu Thr Pro Ile  
 35 40 45  
 Ala Ser Glu Phe Glu Gln Lys Val His Ile Ser Glu Pro Glu Pro Glu  
 50 55 60  
 Val Lys His Glu Ser Leu Leu Glu Lys Leu His Arg Ser Asp Ser Ser  
 65 70 75 80  
 Ser Ser Ser Ser Ser Glu Glu Glu Gly Ser Asp Gly Glu Lys Arg Lys  
 85 90 95  
 Lys Lys Lys Glu Lys Lys Lys Pro Thr Thr Glu Val Glu Val Lys Glu  
 100 105 110  
 Glu Glu Lys Lys Gly Phe Met Glu Lys Leu Lys Glu Lys Leu Pro Gly  
 115 120 125  
 His Lys Lys Pro Glu Asp Gly Ser Ala Val Ala Ala Ala Pro Val Val  
 130 135 140  
 Val Pro Pro Pro Val Glu Glu Ala His Pro Val Glu Lys Lys Gly Ile  
 145 150 155 160  
 Leu Glu Lys Ile Lys Glu Lys Leu Pro Gly Tyr His Pro Lys Thr Thr  
 165 170 175  
 Val Glu Glu Glu Lys Lys Asp Lys Glu  
 180 185

<210> 81  
 <211> 1376  
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<220>  
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 <222> (20)..(1366)

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 1 5 10  
 gag gtt gcg gcg agg cta gcg gct gag gac ttg cat gac att aac aaa 100  
 Glu Val Ala Ala Arg Leu Ala Ala Glu Asp Leu His Asp Ile Asn Lys  
 15 20 25  
 tcc ggt ggt gct gat gtc aca atg tat aag gtg acg gag aga aca act 148



Ser	Gly	Gly	Ala	Asp	Val	Thr	Met	Tyr	Lys	Val	Thr	Glu	Arg	Thr	Thr	
		30					35					40				
gaa	cat	cca	ccg	gag	caa	gat	agg	ccc	ggg	gtg	ata	ggg	tca	gtg	ttc	196
Glu	His	Pro	Pro	Glu	Gln	Asp	Arg	Pro	Gly	Val	Ile	Gly	Ser	Val	Phe	
	45					50				55						
agg	gct	gtc	caa	gga	acg	tat	gag	cat	gcg	aga	gac	gct	gta	gtt	gga	244
Arg	Ala	Val	Gln	Gly	Thr	Tyr	Glu	His	Ala	Arg	Asp	Ala	Val	Val	Gly	
	60				65				70					75		
aaa	acc	cac	gaa	gcg	gct	gag	tct	acc	aaa	gaa	gga	gct	cag	ata	gct	292
Lys	Thr	His	Glu	Ala	Ala	Glu	Ser	Thr	Lys	Glu	Gly	Ala	Gln	Ile	Ala	
			80					85					90			
tca	gag	aaa	gcg	gtt	gga	gca	aag	gac	gca	acc	gtc	gag	aaa	gct	aag	340
Ser	Glu	Lys	Ala	Val	Gly	Ala	Lys	Asp	Ala	Thr	Val	Glu	Lys	Ala	Lys	
		95						100					105			
gaa	acc	gct	gat	tat	act	gcg	gag	aag	gtg	ggg	gag	tat	aaa	gac	tat	388
Glu	Thr	Ala	Asp	Tyr	Thr	Ala	Glu	Lys	Val	Gly	Glu	Tyr	Lys	Asp	Tyr	
	110					115						120				
acg	gtt	gat	aaa	gct	aaa	gag	gct	aag	gac	aca	act	gca	gag	aag	gcg	436
Thr	Val	Asp	Lys	Ala	Lys	Glu	Ala	Lys	Asp	Thr	Thr	Ala	Glu	Lys	Ala	
	125					130					135					
aag	gag	act	gct	aat	tat	act	gcg	gat	aag	gcg	gtg	gaa	gca	aag	gat	484
Lys	Glu	Thr	Ala	Asn	Tyr	Thr	Ala	Asp	Lys	Ala	Val	Glu	Ala	Lys	Asp	
	140				145					150					155	
aag	acg	gcg	gag	aag	att	ggg	gag	tac	aaa	gac	tat	gcg	gtg	gat	aag	532
Lys	Thr	Ala	Glu	Lys	Ile	Gly	Glu	Tyr	Lys	Asp	Tyr	Ala	Val	Asp	Lys	
			160					165						170		
gca	gta	gaa	gct	aaa	gat	aag	aca	gcg	gag	aag	gcg	aag	gag	act	tcg	580
Ala	Val	Glu	Ala	Lys	Asp	Lys	Thr	Ala	Glu	Lys	Ala	Lys	Glu	Thr	Ser	
		175						180					185			
aat	tat	acg	gcg	gat	aag	gct	aaa	gag	gct	aag	gac	aag	acg	gct	gag	628
Asn	Tyr	Thr	Ala	Asp	Lys	Ala	Lys	Glu	Ala	Lys	Asp	Lys	Thr	Ala	Glu	
	190					195						200				
aag	gtt	ggg	gag	tat	aag	gat	tac	acg	gtg	gac	aag	gcc	gtg	gaa	gct	676
Lys	Val	Gly	Glu	Tyr	Lys	Asp	Tyr	Thr	Val	Asp	Lys	Ala	Val	Glu	Ala	
	205					210				215						
agg	gat	tac	aca	gcg	gag	aag	gct	att	gaa	gca	aag	gat	aag	aca	gct	724
Arg	Asp	Tyr	Thr	Ala	Glu	Lys	Ala	Ile	Glu	Ala	Lys	Asp	Lys	Thr	Ala	
	220				225					230					235	
gag	aag	act	gga	gag	tat	aag	gac	tat	acg	gtg	gag	aag	gcg	acg	gag	772
Glu	Lys	Thr	Gly	Glu	Tyr	Lys	Asp	Tyr	Thr	Val	Glu	Lys	Ala	Thr	Glu	
			240					245					250			
ggg	aaa	gat	gtt	acg	gtg	agt	aag	cta	gga	gag	ctg	aag	gat	agt	gcc	820
Gly	Lys	Asp	Val	Thr	Val	Ser	Lys	Leu	Gly	Glu	Leu	Lys	Asp	Ser	Ala	

255	260	265	
gtt gag aca gcg aag aga gct atg ggt ttc ttg tcg ggg aag aca gag Val Glu Thr Ala Lys Arg Ala Met Gly Phe Leu Ser Gly Lys Thr Glu 270 275 280			868
gag gcc aaa gga aaa gct gtg gag acc aaa gat act gcc aag gaa aac Glu Ala Lys Gly Lys Ala Val Glu Thr Lys Asp Thr Ala Lys Glu Asn 285 290 295			916
atg gag aaa gct gga gaa gta aca aga caa aag atg gag gaa atg aga Met Glu Lys Ala Gly Glu Val Thr Arg Gln Lys Met Glu Glu Met Arg 300 305 310 315			964
ttg gaa ggt aaa gag ctc aaa gaa gaa gct gga gca aaa gcc caa gag Leu Glu Gly Lys Glu Leu Lys Glu Glu Ala Gly Ala Lys Ala Gln Glu 320 325 330			1012
gca tct caa aag act agg gag agt act gag tcg gga gct caa aaa gcc Ala Ser Gln Lys Thr Arg Glu Ser Thr Glu Ser Gly Ala Gln Lys Ala 335 340 345			1060
gaa gag acc aaa gat tct cct gcc gtg agg gga aat gaa gcg aaa ggg Glu Glu Thr Lys Asp Ser Pro Ala Val Arg Gly Asn Glu Ala Lys Gly 350 355 360			1108
act att ttt ggt gca tta ggg aat gta acg gaa gca ata aag agc aaa Thr Ile Phe Gly Ala Leu Gly Asn Val Thr Glu Ala Ile Lys Ser Lys 365 370 375			1156
ctg aca atg cca tca gac att gtg gag gaa aca cgc gcg gca cgt gag Leu Thr Met Pro Ser Asp Ile Val Glu Glu Thr Arg Ala Ala Arg Glu 380 385 390 395			1204
cat gga ggg acg ggt agg act gtg gtt gaa gtc aag gtc gag gat tca His Gly Gly Thr Gly Arg Thr Val Val Glu Val Lys Val Glu Asp Ser 400 405 410			1252
aag ccg ggt aag gtg gcg act tca ctg aag gcg tcg gat caa atg acc Lys Pro Gly Lys Val Ala Thr Ser Leu Lys Ala Ser Asp Gln Met Thr 415 420 425			1300
ggt caa aca ttc aac gac gtt gga cgg atg gat gat gat gct cgg aaa Gly Gln Thr Phe Asn Asp Val Gly Arg Met Asp Asp Asp Ala Arg Lys 430 435 440			1348
gat aag gga aag ctg tga gaatactaga Asp Lys Gly Lys Leu 445			1376

&lt;210&gt; 82

&lt;211&gt; 448

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 82

Met Ala Ser Asp Lys Gln Lys Ala Glu Arg Ala Glu Val Ala Ala Arg  
 1 5 10 15  
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 20 25 30  
 Val Thr Met Tyr Lys Val Thr Glu Arg Thr Thr Glu His Pro Pro Glu  
 35 40 45  
 Gln Asp Arg Pro Gly Val Ile Gly Ser Val Phe Arg Ala Val Gln Gly  
 50 55 60  
 Thr Tyr Glu His Ala Arg Asp Ala Val Val Gly Lys Thr His Glu Ala  
 65 70 75 80  
 Ala Glu Ser Thr Lys Glu Gly Ala Gln Ile Ala Ser Glu Lys Ala Val  
 85 90 95  
 Gly Ala Lys Asp Ala Thr Val Glu Lys Ala Lys Glu Thr Ala Asp Tyr  
 100 105 110  
 Thr Ala Glu Lys Val Gly Glu Tyr Lys Asp Tyr Thr Val Asp Lys Ala  
 115 120 125  
 Lys Glu Ala Lys Asp Thr Thr Ala Glu Lys Ala Lys Glu Thr Ala Asn  
 130 135 140  
 Tyr Thr Ala Asp Lys Ala Val Glu Ala Lys Asp Lys Thr Ala Glu Lys  
 145 150 155 160  
 Ile Gly Glu Tyr Lys Asp Tyr Ala Val Asp Lys Ala Val Glu Ala Lys  
 165 170 175  
 Asp Lys Thr Ala Glu Lys Ala Lys Glu Thr Ser Asn Tyr Thr Ala Asp  
 180 185 190  
 Lys Ala Lys Glu Ala Lys Asp Lys Thr Ala Glu Lys Val Gly Glu Tyr  
 195 200 205  
 Lys Asp Tyr Thr Val Asp Lys Ala Val Glu Ala Arg Asp Tyr Thr Ala  
 210 215 220  
 Glu Lys Ala Ile Glu Ala Lys Asp Lys Thr Ala Glu Lys Thr Gly Glu  
 225 230 235 240  
 Tyr Lys Asp Tyr Thr Val Glu Lys Ala Thr Glu Gly Lys Asp Val Thr  
 245 250 255  
 Val Ser Lys Leu Gly Glu Leu Lys Asp Ser Ala Val Glu Thr Ala Lys  
 260 265 270  
 Arg Ala Met Gly Phe Leu Ser Gly Lys Thr Glu Glu Ala Lys Gly Lys  
 275 280 285  
 Ala Val Glu Thr Lys Asp Thr Ala Lys Glu Asn Met Glu Lys Ala Gly  
 290 295 300

Glu Val Thr Arg Gln Lys Met Glu Glu Met Arg Leu Glu Gly Lys Glu  
 305 310 315 320  
 Leu Lys Glu Glu Ala Gly Ala Lys Ala Gln Glu Ala Ser Gln Lys Thr  
 325 330 335  
 Arg Glu Ser Thr Glu Ser Gly Ala Gln Lys Ala Glu Glu Thr Lys Asp  
 340 345 350  
 Ser Pro Ala Val Arg Gly Asn Glu Ala Lys Gly Thr Ile Phe Gly Ala  
 355 360 365  
 Leu Gly Asn Val Thr Glu Ala Ile Lys Ser Lys Leu Thr Met Pro Ser  
 370 375 380  
 Asp Ile Val Glu Glu Thr Arg Ala Ala Arg Glu His Gly Gly Thr Gly  
 385 390 395 400  
 Arg Thr Val Val Glu Val Lys Val Glu Asp Ser Lys Pro Gly Lys Val  
 405 410 415  
 Ala Thr Ser Leu Lys Ala Ser Asp Gln Met Thr Gly Gln Thr Phe Asn  
 420 425 430  
 Asp Val Gly Arg Met Asp Asp Asp Ala Arg Lys Asp Lys Gly Lys Leu  
 435 440 445

<210> 83  
 <211> 561  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> CDS  
 <222> (18) .. (548)

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 1 5 10  
 atc gta gta gca tta ttc ttc gat tta act caa gcc tat cgt cac act 98  
 Ile Val Val Ala Leu Phe Phe Asp Leu Thr Gln Ala Tyr Arg His Thr  
 15 20 25  
 ccc gct caa ccg cca aaa gca aac gca aac ggt gat gtc aaa ccg caa 146  
 Pro Ala Gln Pro Pro Lys Ala Asn Ala Asn Gly Asp Val Lys Pro Gln  
 30 35 40  
 gaa acg ctc gtg gtt cac aac aag gcc cga gcc atg gtc gga gtc gga 194  
 Glu Thr Leu Val Val His Asn Lys Ala Arg Ala Met Val Gly Val Gly  
 45 50 55  
 cca atg gtg tgg aac gaa act ctt gcg acc tat gca cag agc tac gca 242  
 Pro Met Val Trp Asn Glu Thr Leu Ala Thr Tyr Ala Gln Ser Tyr Ala

60	65	70	75	
cat gaa cga gcc aga gac tgt gcc atg aag cat tcc ttg gga cca ttc				290
His Glu Arg Ala Arg Asp Cys Ala Met Lys His Ser Leu Gly Pro Phe	80	85	90	
ggc gag aat cta gcc gcg ggt tgg gga acg atg agc ggt ccg gta gca				338
Gly Glu Asn Leu Ala Ala Gly Trp Gly Thr Met Ser Gly Pro Val Ala	95	100	105	
act gag tat tgg atg acg gag aag gaa aat tac gat tat gat agt aac				386
Thr Glu Tyr Trp Met Thr Glu Lys Glu Asn Tyr Asp Tyr Asp Ser Asn	110	115	120	
acg tgt ggt ggt gat ggt gtg tgt gga cac tac act cag atc gtg tgg				434
Thr Cys Gly Gly Asp Gly Val Cys Gly His Tyr Thr Gln Ile Val Trp	125	130	135	
cgt gac tcg gtt cga ctt ggt tgt gcc tcc gtg aga tgt aag aat gat				482
Arg Asp Ser Val Arg Leu Gly Cys Ala Ser Val Arg Cys Lys Asn Asp	140	145	150	155
gag tat att tgg gtg att tgt agc tat gat cct ccg ggg aat tac atc				530
Glu Tyr Ile Trp Val Ile Cys Ser Tyr Asp Pro Pro Gly Asn Tyr Ile	160	165	170	
ggc caa cgt cca tat tag tgattggatt tta				561
Gly Gln Arg Pro Tyr	175			

&lt;210&gt; 84

&lt;211&gt; 176

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 84

Met Asn Glu Met Ser Phe Phe Gly Tyr Ser Phe Ile Val Val Ala Leu	1	5	10	15
Phe Phe Asp Leu Thr Gln Ala Tyr Arg His Thr Pro Ala Gln Pro Pro	20	25	30	
Lys Ala Asn Ala Asn Gly Asp Val Lys Pro Gln Glu Thr Leu Val Val	35	40	45	
His Asn Lys Ala Arg Ala Met Val Gly Val Gly Pro Met Val Trp Asn	50	55	60	
Glu Thr Leu Ala Thr Tyr Ala Gln Ser Tyr Ala His Glu Arg Ala Arg	65	70	75	80
Asp Cys Ala Met Lys His Ser Leu Gly Pro Phe Gly Glu Asn Leu Ala	85	90	95	
Ala Gly Trp Gly Thr Met Ser Gly Pro Val Ala Thr Glu Tyr Trp Met	100	105	110	

Thr Glu Lys Glu Asn Tyr Asp Tyr Asp Ser Asn Thr Cys Gly Gly Asp  
 115 120 125

Gly Val Cys Gly His Tyr Thr Gln Ile Val Trp Arg Asp Ser Val Arg  
 130 135 140

Leu Gly Cys Ala Ser Val Arg Cys Lys Asn Asp Glu Tyr Ile Trp Val  
 145 150 155 160

Ile Cys Ser Tyr Asp Pro Pro Gly Asn Tyr Ile Gly Gln Arg Pro Tyr  
 165 170 175

<210> 85  
 <211> 988  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
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 <222> (12)..(977)

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tta gtt ttg ttg ttt gct caa gcc aat tcg caa ggt ttg aaa gta ggt 98  
 Leu Val Leu Leu Phe Ala Gln Ala Asn Ser Gln Gly Leu Lys Val Gly  
 15 20 25

ttc tac agc aaa aca tgc cca caa ctc gag ggt ata gtt aaa aag gtc 146  
 Phe Tyr Ser Lys Thr Cys Pro Gln Leu Glu Gly Ile Val Lys Lys Val  
 30 35 40 45

gtg ttc gat gcg atg aac aaa gca cca aca ctt ggt gct cct ttg ctt 194  
 Val Phe Asp Ala Met Asn Lys Ala Pro Thr Leu Gly Ala Pro Leu Leu  
 50 55 60

aga atg ttc ttc cac gac tgc ttc gtt cgg gga tgt gac gga tca gtt 242  
 Arg Met Phe Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val  
 65 70 75

ttg tta gat aaa cca aac aat caa ggt gag aag agt gca gtt cct aac 290  
 Leu Leu Asp Lys Pro Asn Asn Gln Gly Glu Lys Ser Ala Val Pro Asn  
 80 85 90

cta agt ctt cga ggg ttt ggc atc ata gac gat tcc aag gcg gct cta 338  
 Leu Ser Leu Arg Gly Phe Gly Ile Ile Asp Asp Ser Lys Ala Ala Leu  
 95 100 105

gaa aaa gtg tgt ccg gga att gtt tct tgc tct gat atc ttg gca ctt 386  
 Glu Lys Val Cys Pro Gly Ile Val Ser Cys Ser Asp Ile Leu Ala Leu  
 110 115 120 125



gtc gct aga gac gca atg gtt gca ctt gaa gga cca tca tgg gaa gtt 434  
 Val Ala Arg Asp Ala Met Val Ala Leu Glu Gly Pro Ser Trp Glu Val  
 130 135 140

gaa acg gga aga aga gac ggt agg gtt tct aac atc aac gaa gtc aac 482  
 Glu Thr Gly Arg Arg Asp Gly Arg Val Ser Asn Ile Asn Glu Val Asn  
 145 150 155

ttg cca tca cct ttt gat aac atc acc aag ctt atc agc gat ttt cgc 530  
 Leu Pro Ser Pro Phe Asp Asn Ile Thr Lys Leu Ile Ser Asp Phe Arg  
 160 165 170

tca aag ggc ctc aac gag aag gat cta gtc att ctc tcg ggt ggt cac 578  
 Ser Lys Gly Leu Asn Glu Lys Asp Leu Val Ile Leu Ser Gly Gly His  
 175 180 185

aca att gga atg gga cat tgt cct tta ttg aca aac cgg ctt tac aac 626  
 Thr Ile Gly Met Gly His Cys Pro Leu Leu Thr Asn Arg Leu Tyr Asn  
 190 195 200 205

ttc acc gga aaa gga gac agc gac cca agt ttg gac tcg gag tac gcc 674  
 Phe Thr Gly Lys Gly Asp Ser Asp Pro Ser Leu Asp Ser Glu Tyr Ala  
 210 215 220

gct aag ctc agg aag aaa tgc aag ccc acc gat acg acg acg gct cta 722  
 Ala Lys Leu Arg Lys Lys Cys Lys Pro Thr Asp Thr Thr Thr Ala Leu  
 225 230 235

gag atg gat ccg ggg agt ttc aaa aca ttt gac ttg agc tac ttc acg 770  
 Glu Met Asp Pro Gly Ser Phe Lys Thr Phe Asp Leu Ser Tyr Phe Thr  
 240 245 250

cta gtg gct aag aga aga gga ctt ttc cag tcg gat gct gct cta ctc 818  
 Leu Val Ala Lys Arg Arg Gly Leu Phe Gln Ser Asp Ala Ala Leu Leu  
 255 260 265

gac aac tcc aag act agg gct tat gtc ttg caa cag ata aga act cat 866  
 Asp Asn Ser Lys Thr Arg Ala Tyr Val Leu Gln Gln Ile Arg Thr His  
 270 275 280 285

ggg tca atg ttc ttt aac gac ttt ggt gtc tct atg gtg aaa atg ggt 914  
 Gly Ser Met Phe Phe Asn Asp Phe Gly Val Ser Met Val Lys Met Gly  
 290 295 300

cgg act gga gtt ctt acg ggt aag gcc ggg gag atc cgt aag acg tgt 962  
 Arg Thr Gly Val Leu Thr Gly Lys Ala Gly Glu Ile Arg Lys Thr Cys  
 305 310 315

cgg tct gct aat taa gagatataga aa 989  
 Arg Ser Ala Asn  
 320

&lt;210&gt; 86

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 86

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 Lys Thr Cys Pro Gln Leu Glu Gly Ile Val Lys Lys Val Val Phe Asp  
 35 40 45  
 Ala Met Asn Lys Ala Pro Thr Leu Gly Ala Pro Leu Leu Arg Met Phe  
 50 55 60  
 Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Leu Asp  
 65 70 75 80  
 Lys Pro Asn Asn Gln Gly Glu Lys Ser Ala Val Pro Asn Leu Ser Leu  
 85 90 95  
 Arg Gly Phe Gly Ile Ile Asp Asp Ser Lys Ala Ala Leu Glu Lys Val  
 100 105 110  
 Cys Pro Gly Ile Val Ser Cys Ser Asp Ile Leu Ala Leu Val Ala Arg  
 115 120 125  
 Asp Ala Met Val Ala Leu Glu Gly Pro Ser Trp Glu Val Glu Thr Gly  
 130 135 140  
 Arg Arg Asp Gly Arg Val Ser Asn Ile Asn Glu Val Asn Leu Pro Ser  
 145 150 155 160  
 Pro Phe Asp Asn Ile Thr Lys Leu Ile Ser Asp Phe Arg Ser Lys Gly  
 165 170 175  
 Leu Asn Glu Lys Asp Leu Val Ile Leu Ser Gly Gly His Thr Ile Gly  
 180 185 190  
 Met Gly His Cys Pro Leu Leu Thr Asn Arg Leu Tyr Asn Phe Thr Gly  
 195 200 205  
 Lys Gly Asp Ser Asp Pro Ser Leu Asp Ser Glu Tyr Ala Ala Lys Leu  
 210 215 220  
 Arg Lys Lys Cys Lys Pro Thr Asp Thr Thr Thr Ala Leu Glu Met Asp  
 225 230 235 240  
 Pro Gly Ser Phe Lys Thr Phe Asp Leu Ser Tyr Phe Thr Leu Val Ala  
 245 250 255  
 Lys Arg Arg Gly Leu Phe Gln Ser Asp Ala Ala Leu Leu Asp Asn Ser  
 260 265 270  
 Lys Thr Arg Ala Tyr Val Leu Gln Gln Ile Arg Thr His Gly Ser Met  
 275 280 285  
 Phe Phe Asn Asp Phe Gly Val Ser Met Val Lys Met Gly Arg Thr Gly

290	295	300	
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Asn			
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tcg ttc tcc tcc caa gtt tct caa aga cct aac acc att tcc ttc ccc			97
Ser Phe Ser Ser Gln Val Ser Gln Arg Pro Asn Thr Ile Ser Phe Pro			
15	20	25	30
cgc gcg aat tca gta ttc gca tta ccg gcg aaa tcc gca cgc cgc gct			145
Arg Ala Asn Ser Val Phe Ala Leu Pro Ala Lys Ser Ala Arg Arg Ala			
35	40	45	
tct cta tct atc acc gcc acg gta tct gct cca ccg gag gag gag gag			193
Ser Leu Ser Ile Thr Ala Thr Val Ser Ala Pro Pro Glu Glu Glu Glu			
50	55	60	
ata gtt gaa ctg aag aaa tac gtc aaa tcg agg ctt ccc gga gga ttt			241
Ile Val Glu Leu Lys Lys Tyr Val Lys Ser Arg Leu Pro Gly Gly Phe			
65	70	75	
gct gct cag aag att att ggc act gga cga cgt aag tgc gca atc gct			289
Ala Ala Gln Lys Ile Ile Gly Thr Gly Arg Arg Lys Cys Ala Ile Ala			
80	85	90	
aga gtt gtt ctt cag gaa ggt act ggg aag gtt atc atc aac tat cgt			337
Arg Val Val Leu Gln Glu Gly Thr Gly Lys Val Ile Ile Asn Tyr Arg			
95	100	105	110
gat gcc aag gag tac ctt cag gga aat cca ttg tgg ctt cag tat gtt			385
Asp Ala Lys Glu Tyr Leu Gln Gly Asn Pro Leu Trp Leu Gln Tyr Val			
115	120	125	
aaa gta cca ttg gtg act tta gga tat gag aat agc tac gac ata ttt			433
Lys Val Pro Leu Val Thr Leu Gly Tyr Glu Asn Ser Tyr Asp Ile Phe			
130	135	140	
gtg aaa gcc cat gga ggc ggt ctc tca ggt caa gct caa gca att acc			481
Val Lys Ala His Gly Gly Gly Leu Ser Gly Gln Ala Gln Ala Ile Thr			

145	150	155	
ttg gga gtc gca cgt gca ctc ctg aag gta agt gca gac cac aga tcg			529
Leu Gly Val Ala Arg Ala Leu Leu Lys Val Ser Ala Asp His Arg Ser			
160	165	170	
cct ttg aag aag gaa ggt ttg ctc act aga gat gcg aga gtg gtt gaa			577
Pro Leu Lys Lys Glu Gly Leu Leu Thr Arg Asp Ala Arg Val Val Glu			
175	180	185	190
aga aag aag gcc ggg ctc aag aag gcg cgt aaa gcc cca caa ttc tcc			625
Arg Lys Lys Ala Gly Leu Lys Lys Ala Arg Lys Ala Pro Gln Phe Ser			
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Lys Arg			
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Asn Ser Val Phe Ala Leu Pro Ala Lys Ser Ala Arg Arg Ala Ser Leu			
35	40	45	
Ser Ile Thr Ala Thr Val Ser Ala Pro Pro Glu Glu Glu Glu Ile Val			
50	55	60	
Glu Leu Lys Lys Tyr Val Lys Ser Arg Leu Pro Gly Gly Phe Ala Ala			
65	70	75	80
Gln Lys Ile Ile Gly Thr Gly Arg Arg Lys Cys Ala Ile Ala Arg Val			
85	90	95	
Val Leu Gln Glu Gly Thr Gly Lys Val Ile Ile Asn Tyr Arg Asp Ala			
100	105	110	
Lys Glu Tyr Leu Gln Gly Asn Pro Leu Trp Leu Gln Tyr Val Lys Val			
115	120	125	
Pro Leu Val Thr Leu Gly Tyr Glu Asn Ser Tyr Asp Ile Phe Val Lys			
130	135	140	
Ala His Gly Gly Gly Leu Ser Gly Gln Ala Gln Ala Ile Thr Leu Gly			
145	150	155	160
Val Ala Arg Ala Leu Leu Lys Val Ser Ala Asp His Arg Ser Pro Leu			
165	170	175	

Lys Lys Glu Gly Leu Leu Thr Arg Asp Ala Arg Val Val Glu Arg Lys  
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Lys Ala Gly Leu Lys Lys Ala Arg Lys Ala Pro Gln Phe Ser Lys Arg  
 195 200 205

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gag atg gct cgg act cag aag aat aaa gct aca gag tat cat ctt ggt 99  
 Glu Met Ala Arg Thr Gln Lys Asn Lys Ala Thr Glu Tyr His Leu Gly  
 15 20 25

cag ctc aag gca aag att gca aaa ctc agg aca caa ctg ttg gag cct 147  
 Gln Leu Lys Ala Lys Ile Ala Lys Leu Arg Thr Gln Leu Leu Glu Pro  
 30 35 40

cca aaa ggt gct agt gga ggc ggg gaa ggt ttt gaa gtt acc aag tat 195  
 Pro Lys Gly Ala Ser Gly Gly Gly Glu Gly Phe Glu Val Thr Lys Tyr  
 45 50 55 60

ggt cat gga cgt gtt gca ctt ata gga ttt cct agt gtc gga aag tcc 243  
 Gly His Gly Arg Val Ala Leu Ile Gly Phe Pro Ser Val Gly Lys Ser  
 65 70 75

acg ctt ttg act atg tta act gga aca cat tct gaa gca gcc tca tat 291  
 Thr Leu Leu Thr Met Leu Thr Gly Thr His Ser Glu Ala Ala Ser Tyr  
 80 85 90

gaa ttt aca aca ctt aca tgc atc cct ggt gta att cac tac aac gac 339  
 Glu Phe Thr Thr Leu Thr Cys Ile Pro Gly Val Ile His Tyr Asn Asp  
 95 100 105

aca aag att cag ctt ctc gat ctt cct ggg att att gaa ggt gct tcg 387  
 Thr Lys Ile Gln Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ser  
 110 115 120

gaa gga aag ggg cga gga agg cag gtt att gct gtt gca aag tct tcc 435  
 Glu Gly Lys Gly Arg Gly Arg Gln Val Ile Ala Val Ala Lys Ser Ser  
 125 130 135 140

gac ctt gta ttg atg gtt ctt gat gcc tca aaa agc gaa ggc cac agg 483  
 Asp Leu Val Leu Met Val Leu Asp Ala Ser Lys Ser Glu Gly His Arg  
 145 150 155

caa ata ttg act aag gaa ctt gag gca gtg ggc ttg cga cta aac aaa	531
Gln Ile Leu Thr Lys Glu Leu Glu Ala Val Gly Leu Arg Leu Asn Lys	
160 165 170	
act cct ccg cag ata tac ttt aaa aag aaa aag act ggt gga atc tct	579
Thr Pro Pro Gln Ile Tyr Phe Lys Lys Lys Lys Thr Gly Gly Ile Ser	
175 180 185	
ttc aac act aca gca ccc ttg act cac att gat gag aag ctc tgt tat	627
Phe Asn Thr Thr Ala Pro Leu Thr His Ile Asp Glu Lys Leu Cys Tyr	
190 195 200	
caa atc ctg cat gaa tac aag att cac aat gct gag gtg cta ttt cgt	675
Gln Ile Leu His Glu Tyr Lys Ile His Asn Ala Glu Val Leu Phe Arg	
205 210 215 220	
gag aat gcc aca gtg gat gac ttt att gat gtc att gaa ggc aac cgc	723
Glu Asn Ala Thr Val Asp Asp Phe Ile Asp Val Ile Glu Gly Asn Arg	
225 230 235	
aag tat att aag tgt gtt tat gtc tac atc aaa ata gat gtt gtt gga	771
Lys Tyr Ile Lys Cys Val Tyr Val Tyr Ile Lys Ile Asp Val Val Gly	
240 245 250	
att gat gat gtg gat aga cta tcc cgg cag cca aat tcc att gtt att	819
Ile Asp Asp Val Asp Arg Leu Ser Arg Gln Pro Asn Ser Ile Val Ile	
255 260 265	
agc tgc aat ctt aag ctt aac tta gac aga cta ctt gct agg atg tgg	867
Ser Cys Asn Leu Lys Leu Asn Leu Asp Arg Leu Leu Ala Arg Met Trp	
270 275 280	
gac gaa atg ggc ctt gtg aga gtt tac tcg aag ccg caa ggc cag caa	915
Asp Glu Met Gly Leu Val Arg Val Tyr Ser Lys Pro Gln Gly Gln Gln	
285 290 295 300	
cca gat ttc gat gag cct ttt gtc ctc tca tct gat cga ggt ggc tgc	963
Pro Asp Phe Asp Glu Pro Phe Val Leu Ser Ser Asp Arg Gly Gly Cys	
305 310 315	
aca gtg gaa gac ttc tgt aac cac gtc cac agg act ctg gtg aag gat	1011
Thr Val Glu Asp Phe Cys Asn His Val His Arg Thr Leu Val Lys Asp	
320 325 330	
atg aag tat gca ctc gtt tgg ggc aca agc aca agg cac aat cca cag	1059
Met Lys Tyr Ala Leu Val Trp Gly Thr Ser Thr Arg His Asn Pro Gln	
335 340 345	
aat tgt ggt ctt tct caa cat ctt gaa gac gaa gat gtt gtt cag atc	1107
Asn Cys Gly Leu Ser Gln His Leu Glu Asp Glu Asp Val Val Gln Ile	
350 355 360	
gtc aag aaa aag gag aga gac gaa gga gga aga ggc cgg ttc aag tca	1155
Val Lys Lys Lys Glu Arg Asp Glu Gly Gly Arg Gly Arg Phe Lys Ser	
365 370 375 380	



cac tca aac gcc cct gct aga att gca gac aga gag aaa aaa gct cct 1203  
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 Leu Lys Gln  
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Lys Ile Ala Lys Leu Arg Thr Gln Leu Leu Glu Pro Pro Lys Gly Ala  
 35 40 45

Ser Gly Gly Gly Glu Gly Phe Glu Val Thr Lys Tyr Gly His Gly Arg  
 50 55 60

Val Ala Leu Ile Gly Phe Pro Ser Val Gly Lys Ser Thr Leu Leu Thr  
 65 70 75 80

Met Leu Thr Gly Thr His Ser Glu Ala Ala Ser Tyr Glu Phe Thr Thr  
 85 90 95

Leu Thr Cys Ile Pro Gly Val Ile His Tyr Asn Asp Thr Lys Ile Gln  
 100 105 110

Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ser Glu Gly Lys Gly  
 115 120 125

Arg Gly Arg Gln Val Ile Ala Val Ala Lys Ser Ser Asp Leu Val Leu  
 130 135 140

Met Val Leu Asp Ala Ser Lys Ser Glu Gly His Arg Gln Ile Leu Thr  
 145 150 155 160

Lys Glu Leu Glu Ala Val Gly Leu Arg Leu Asn Lys Thr Pro Pro Gln  
 165 170 175

Ile Tyr Phe Lys Lys Lys Lys Thr Gly Gly Ile Ser Phe Asn Thr Thr  
 180 185 190

Ala Pro Leu Thr His Ile Asp Glu Lys Leu Cys Tyr Gln Ile Leu His  
 195 200 205

Glu Tyr Lys Ile His Asn Ala Glu Val Leu Phe Arg Glu Asn Ala Thr  
 210 215 220

Val Asp Asp Phe Ile Asp Val Ile Glu Gly Asn Arg Lys Tyr Ile Lys  
 225 230 235 240  
 Cys Val Tyr Val Tyr Ile Lys Ile Asp Val Val Gly Ile Asp Asp Val  
 245 250 255  
 Asp Arg Leu Ser Arg Gln Pro Asn Ser Ile Val Ile Ser Cys Asn Leu  
 260 265 270  
 Lys Leu Asn Leu Asp Arg Leu Leu Ala Arg Met Trp Asp Glu Met Gly  
 275 280 285  
 Leu Val Arg Val Tyr Ser Lys Pro Gln Gly Gln Gln Pro Asp Phe Asp  
 290 295 300  
 Glu Pro Phe Val Leu Ser Ser Asp Arg Gly Gly Cys Thr Val Glu Asp  
 305 310 315 320  
 Phe Cys Asn His Val His Arg Thr Leu Val Lys Asp Met Lys Tyr Ala  
 325 330 335  
 Leu Val Trp Gly Thr Ser Thr Arg His Asn Pro Gln Asn Cys Gly Leu  
 340 345 350  
 Ser Gln His Leu Glu Asp Glu Asp Val Val Gln Ile Val Lys Lys Lys  
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 Glu Arg Asp Glu Gly Gly Arg Gly Arg Phe Lys Ser His Ser Asn Ala  
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 gtc tac ggc agt ttc caa gaa cca gcc gtt gtt aat tta att ctc gaa 98  
 Val Tyr Gly Ser Phe Gln Glu Pro Ala Val Val Asn Leu Ile Leu Glu  
 15 20 25  
 tgt gct ccg gtc atg gtt tcc gct caa ctc cac ggc tat cac ttg tat 146  
 Cys Ala Pro Val Met Val Ser Ala Gln Leu His Gly Tyr His Leu Tyr  
 30 35 40 45

aga ctt aaa ggt cgt ttg cat cca tgt att tct cct tcc gac aat gga 194  
 Arg Leu Lys Gly Arg Leu His Pro Cys Ile Ser Pro Ser Asp Asn Gly  
                     50                    55                    60

tta atc aat ggc aag ata cta act gga tta aca gat tct cag tta gag 242  
 Leu Ile Asn Gly Lys Ile Leu Thr Gly Leu Thr Asp Ser Gln Leu Glu  
                     65                    70                    75

agt tta gat atg att gaa gga act gaa tat gtg agg aag act gtt gaa 290  
 Ser Leu Asp Met Ile Glu Gly Thr Glu Tyr Val Arg Lys Thr Val Glu  
                     80                    85                    90

gtt gtt ttg act gat act ttg gag aag aag caa gtt gaa aca att gta 338  
 Val Val Leu Thr Asp Thr Leu Glu Lys Lys Gln Val Glu Thr Ile Val  
                     95                    100                    105

tgg gca aac aag gat gat cct aat atg tat gga gaa tgg gat ttc gag 386  
 Trp Ala Asn Lys Asp Asp Pro Asn Met Tyr Gly Glu Trp Asp Phe Glu  
 110                    115                    120                    125

gaa tgg aag agg ctt cat atg gag aaa ttt ata gag gcg gcg acg aaa 434  
 Glu Trp Lys Arg Leu His Met Glu Lys Phe Ile Glu Ala Ala Thr Lys  
                     130                    135                    140

ttc atg gag tgg aag aag aat ccg aat ggg aga agt agg gaa gag ttt 482  
 Phe Met Glu Trp Lys Lys Asn Pro Asn Gly Arg Ser Arg Glu Glu Phe  
                     145                    150                    155

gag aag ttt gta caa gat gat tct tct ccg gct tgc gct tga 524  
 Glu Lys Phe Val Gln Asp Asp Ser Ser Pro Ala Ser Ala  
                     160                    165                    170

agaagttggt ta 536

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Ser Phe Gln Glu Pro Ala Val Val Asn Leu Ile Leu Glu Cys Ala Pro  
                     20                    25                    30

Val Met Val Ser Ala Gln Leu His Gly Tyr His Leu Tyr Arg Leu Lys  
                     35                    40                    45

Gly Arg Leu His Pro Cys Ile Ser Pro Ser Asp Asn Gly Leu Ile Asn  
                     50                    55                    60

Gly Lys Ile Leu Thr Gly Leu Thr Asp Ser Gln Leu Glu Ser Leu Asp  
                     65                    70                    75                    80

Met Ile Glu Gly Thr Glu Tyr Val Arg Lys Thr Val Glu Val Val Leu

	85		90		95
Thr Asp Thr	Leu Glu Lys Lys Gln Val Glu Thr Ile Val Trp Ala Asn				
	100		105		110
Lys Asp Asp	Pro Asn Met Tyr Gly Glu Trp Asp Phe Glu Glu Trp Lys				
	115		120		125
Arg Leu His	Met Glu Lys Phe Ile Glu Ala Ala Thr Lys Phe Met Glu				
	130		135		140
Trp Lys Lys	Asn Pro Asn Gly Arg Ser Arg Glu Glu Phe Glu Lys Phe				
145		150		155	160
Val Gln Asp	Asp Ser Ser Pro Ala Ser Ala				
	165		170		

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 Lys Cys Gly Asp Ser Cys Se  
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atcatgcata tatatcctaa tatacatgtg gttacatatt ccttaagata aattttgaaa 161

tcttataactt ctgttggtttt tttgggtatga caaag t tgc gag aag aac tac aac 215  
 r Cys Glu Lys Asn Tyr Asn  
 20 25

aag gag tgt gat aac tgt agc tgt gga tca aac tgc agc tgc ggg tca 263  
 Lys Glu Cys Asp Asn Cys Ser Cys Gly Ser Asn Cys Ser Cys Gly Ser  
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 Ser Cys Asn Cys  
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                   1                  5                  10  
 cgc ctc aga tct ctc gct ctt tcg tct tct ttt tct tct ttc cga ttt 97  
 Arg Leu Arg Ser Leu Ala Leu Ser Ser Ser Phe Ser Ser Phe Arg Phe  
           15                  20                  25  
 gcc cat cgt cct ctg tca tcg att tca ccg aga aag tta ccg aat ttt 145  
 Ala His Arg Pro Leu Ser Ser Ile Ser Pro Arg Lys Leu Pro Asn Phe  
           30                  35                  40  
 cgt gct ttc tct ggt acc gct atg aca gat act aaa gat gct ggt atg 193  
 Arg Ala Phe Ser Gly Thr Ala Met Thr Asp Thr Lys Asp Ala Gly Met  
   45                  50                  55                  60  
 gat gct gtt cag aga cgt ctc atg ttt gag gat gaa tgc att ctt gtt 241  
 Asp Ala Val Gln Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val  
                   65                  70                  75  
 gat gaa act gat cgt gtt gtg ggg cat gac agc aag tat aat tgt cat 289  
 Asp Glu Thr Asp Arg Val Val Gly His Asp Ser Lys Tyr Asn Cys His  
           80                  85                  90  
 ctg atg gaa aat att gaa gcc aag aat ttg ctg cac agg gct ttt agt 337  
 Leu Met Glu Asn Ile Glu Ala Lys Asn Leu Leu His Arg Ala Phe Ser  
           95                  100                  105  
 gta ttt tta ttc aac tcg aag tat gag ttg ctt ctc cag caa agg tca 385  
 Val Phe Leu Phe Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser  
   110                  115                  120

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aac aca aag gtt acg ttc cct cta gtg tgg act aac act tgt tgc agc 433
Asn Thr Lys Val Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser
125 130 135 140

cat cct ctt tac cgt gaa tca gag ctt atc cag gac aat gca cta ggt 481
His Pro Leu Tyr Arg Glu Ser Glu Leu Ile Gln Asp Asn Ala Leu Gly
145 150 155

gtg agg aat gct gca caa aga aag ctt ctc gat gag ctt ggt att gta 529
Val Arg Asn Ala Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Val
160 165 170

gct gaa gat gta cca gtc gat gag ttc act ccc ttg gga cgt atg ctg 577
Ala Glu Asp Val Pro Val Asp Glu Phe Thr Pro Leu Gly Arg Met Leu
175 180 185

tac aag gct cct tct gat ggc aaa tgg gga gag cat gaa ctt gat tac 625
Tyr Lys Ala Pro Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr
190 195 200

ttg ctc ttc atc gtg cga gac gtg aag gtt caa cca aac cca gat gaa 673
Leu Leu Phe Ile Val Arg Asp Val Lys Val Gln Pro Asn Pro Asp Glu
205 210 215 220

gta gct gag atc aag tat gtg agc cgg gaa gag ctg aag gag ctg gtg 721
Val Ala Glu Ile Lys Tyr Val Ser Arg Glu Glu Leu Lys Glu Leu Val
225 230 235

aag aaa gca gat gca ggt gag gaa ggt ttg aaa ctg tca cca tgg ttc 769
Lys Lys Ala Asp Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe
240 245 250

aga ttg gtg gtg gac aat ttc ttg atg aag tgg tgg gat cat gta gag 817
Arg Leu Val Val Asp Asn Phe Leu Met Lys Trp Trp Asp His Val Glu
255 260 265

aaa gga act ttg gtt gaa gct ata gac atg aaa acc atc cac aaa ctc 865
Lys Gly Thr Leu Val Glu Ala Ile Asp Met Lys Thr Ile His Lys Leu
270 275 280

tga acatcttttt tt 880
285

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&lt;210&gt; 96

&lt;211&gt; 284

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 96

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Leu Ala Leu Ser Ser Ser Phe Ser Ser Phe Arg Phe Ala His Arg Pro
20 25 30

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Leu Ser Ser Ile Ser Pro Arg Lys Leu Pro Asn Phe Arg Ala Phe Ser  
 35 40 45  
 Gly Thr Ala Met Thr Asp Thr Lys Asp Ala Gly Met Asp Ala Val Gln  
 50 55 60  
 Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val Asp Glu Thr Asp  
 65 70 75 80  
 Arg Val Val Gly His Asp Ser Lys Tyr Asn Cys His Leu Met Glu Asn  
 85 90 95  
 Ile Glu Ala Lys Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe  
 100 105 110  
 Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser Asn Thr Lys Val  
 115 120 125  
 Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Tyr  
 130 135 140  
 Arg Glu Ser Glu Leu Ile Gln Asp Asn Ala Leu Gly Val Arg Asn Ala  
 145 150 155 160  
 Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Val Ala Glu Asp Val  
 165 170 175  
 Pro Val Asp Glu Phe Thr Pro Leu Gly Arg Met Leu Tyr Lys Ala Pro  
 180 185 190  
 Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile  
 195 200 205  
 Val Arg Asp Val Lys Val Gln Pro Asn Pro Asp Glu Val Ala Glu Ile  
 210 215 220  
 Lys Tyr Val Ser Arg Glu Glu Leu Lys Glu Leu Val Lys Lys Ala Asp  
 225 230 235 240  
 Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe Arg Leu Val Val  
 245 250 255  
 Asp Asn Phe Leu Met Lys Trp Trp Asp His Val Glu Lys Gly Thr Leu  
 260 265 270  
 Val Glu Ala Ile Asp Met Lys Thr Ile His Lys Leu  
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&lt;222&gt; (18)..(821)

&lt;400&gt; 97

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      Met Ala Ala Ser Thr Met Ala Leu Ser Ser Pro
           1             5             10

gcc ttc gcc ggt aag gcc gtc aag ctt tcc ccc gcg gca tca gaa gtc    98
Ala Phe Ala Gly Lys Ala Val Lys Leu Ser Pro Ala Ala Ser Glu Val
           15             20             25

ctt gga agc ggc cgt gtg aca atg agg aag act gtt gcc aag cca aag    146
Leu Gly Ser Gly Arg Val Thr Met Arg Lys Thr Val Ala Lys Pro Lys
           30             35             40

ggc cca tca ggc agc cca tgg tac gga tct gac cgt gtc aag tac ttg    194
Gly Pro Ser Gly Ser Pro Trp Tyr Gly Ser Asp Arg Val Lys Tyr Leu
           45             50             55

ggt cca ttc tct ggc gaa tca ccg agc tac ctt acc gga gag ttc ccc    242
Gly Pro Phe Ser Gly Glu Ser Pro Ser Tyr Leu Thr Gly Glu Phe Pro
           60             65             70             75

gga gac tac gga tgg gac acc gcc gga ctt tca gct gac ccc gag aca    290
Gly Asp Tyr Gly Trp Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr
           80             85             90

ttc gca agg aac cgt gaa cta gaa gtt atc cac agc agg tgg gct atg    338
Phe Ala Arg Asn Arg Glu Leu Glu Val Ile His Ser Arg Trp Ala Met
           95             100             105

ctc gga gcc cta ggc tgc gtc ttc cct gag ctt ttg gct aga aac gga    386
Leu Gly Ala Leu Gly Cys Val Phe Pro Glu Leu Leu Ala Arg Asn Gly
           110             115             120

gtc aag ttc gga gag gcg gtt tgg ttc aag gcc ggt tca cag atc ttc    434
Val Lys Phe Gly Glu Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe
           125             130             135

agc gat gga ggg ctc gat tac ttg gga aac cct agc ttg gtt cac gct    482
Ser Asp Gly Gly Leu Asp Tyr Leu Gly Asn Pro Ser Leu Val His Ala
           140             145             150             155

cag agc att ttg gcc att tgg gcc aca caa gtt att ttg atg gga gcc    530
Gln Ser Ile Leu Ala Ile Trp Ala Thr Gln Val Ile Leu Met Gly Ala
           160             165             170

gtt gaa ggc tac aga gtc gca gga aat ggg cca ttg gga gag gcc gag    578
Val Glu Gly Tyr Arg Val Ala Gly Asn Gly Pro Leu Gly Glu Ala Glu
           175             180             185

gac ttg ctt tac ccc ggt ggc agc ttc gac cca ttg ggt ttg gct acc    626
Asp Leu Leu Tyr Pro Gly Gly Ser Phe Asp Pro Leu Gly Leu Ala Thr
           190             195             200

gac cca gag gca ttc gct gag ttg aag gtg aag gag ctc aag aac gga    674

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Asp Pro Glu Ala Phe Ala Glu Leu Lys Val Lys Glu Leu Lys Asn Gly  
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 aga ttg gct atg ttc tct atg ttt gga ttc ttc gtt caa gcc atc gtc 722  
 Arg Leu Ala Met Phe Ser Met Phe Gly Phe Phe Val Gln Ala Ile Val  
 220 225 230 235  
 act ggt aag gga ccg ata gag aac ctt gct gac cat ttg gcc gat cca 770  
 Thr Gly Lys Gly Pro Ile Glu Asn Leu Ala Asp His Leu Ala Asp Pro  
 240 245 250  
 gtt aac aac aac gca tgg gcc ttc gcc acc aac ttt gtt ccc gga aag 818  
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 35 40 45  
 Pro Trp Tyr Gly Ser Asp Arg Val Lys Tyr Leu Gly Pro Phe Ser Gly  
 50 55 60  
 Glu Ser Pro Ser Tyr Leu Thr Gly Glu Phe Pro Gly Asp Tyr Gly Trp  
 65 70 75 80  
 Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr Phe Ala Arg Asn Arg  
 85 90 95  
 Glu Leu Glu Val Ile His Ser Arg Trp Ala Met Leu Gly Ala Leu Gly  
 100 105 110  
 Cys Val Phe Pro Glu Leu Leu Ala Arg Asn Gly Val Lys Phe Gly Glu  
 115 120 125  
 Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe Ser Asp Gly Gly Leu  
 130 135 140  
 Asp Tyr Leu Gly Asn Pro Ser Leu Val His Ala Gln Ser Ile Leu Ala  
 145 150 155 160  
 Ile Trp Ala Thr Gln Val Ile Leu Met Gly Ala Val Glu Gly Tyr Arg  
 165 170 175

Val Ala Gly Asn Gly Pro Leu Gly Glu Ala Glu Asp Leu Leu Tyr Pro  
 180 185 190

Gly Gly Ser Phe Asp Pro Leu Gly Leu Ala Thr Asp Pro Glu Ala Phe  
 195 200 205

Ala Glu Leu Lys Val Lys Glu Leu Lys Asn Gly Arg Leu Ala Met Phe  
 210 215 220

Ser Met Phe Gly Phe Phe Val Gln Ala Ile Val Thr Gly Lys Gly Pro  
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 Thr Ala Thr Arg Arg Val Leu Ile Ala Leu His Glu Lys Asn Val Asp  
 15 20 25

ttt gaa ttc gtt cat gtc gag ctc aaa gat ggt gaa cac aag aaa gag 146  
 Phe Glu Phe Val His Val Glu Leu Lys Asp Gly Glu His Lys Lys Glu  
 30 35 40

cct ttc atc ctt cgc aac gtgagtacat ataacatctg tcaagccaaa 194  
 Pro Phe Ile Leu Arg Asn  
 45 50

atattgtatt tcatttagat actgaatctt ggtcttaaca atcttgaata atgtttttgc 254

ag ccc ttt ggt aaa gtt cca gcc ttt gaa gat gga gac ttc aag att 301  
 Pro Phe Gly Lys Val Pro Ala Phe Glu Asp Gly Asp Phe Lys Ile  
 55 60 65

ttc g gtaaatacaa atatatatca ttatagtcac gtttacaat ttttggtttt 355  
 Phe G

atgatcattg caataataga aagcagaaac actcaaaaat gttttttttt tgggtgggcag 415

aa tca aga gca att act caa tac ata gct cat gaa ttc tca gac aaa 462  
 lu Ser Arg Ala Ile Thr Gln Tyr Ile Ala His Glu Phe Ser Asp Lys  
 70 75 80

gga aac aac ctt ctc tca act ggc aag gac atg gcg atc ata gcc atg 510  
 Gly Asn Asn Leu Leu Ser Thr Gly Lys Asp Met Ala Ile Ile Ala Met  
 85 90 95

ggc att gaa att gag tcg cat gag ttt gac cca gtt ggt tca aag ctt 558  
 Gly Ile Glu Ile Glu Ser His Glu Phe Asp Pro Val Gly Ser Lys Leu  
 100 105 110

gtt tgg gag caa gtc tta aag cct ttg tat ggt atg acc aca gac aaa 606  
 Val Trp Glu Gln Val Leu Lys Pro Leu Tyr Gly Met Thr Thr Asp Lys  
 115 120 125

act gtt gtt gaa gaa gaa gag gct aag cta gcc aaa gtc ctc gat gtt 654  
 Thr Val Val Glu Glu Glu Glu Ala Lys Leu Ala Lys Val Leu Asp Val  
 130 135 140 145

tac gaa cac agg ctt ggt gag tcc aag tat ttg gct tct gac cac ttc 702  
 Tyr Glu His Arg Leu Gly Glu Ser Lys Tyr Leu Ala Ser Asp His Phe  
 150 155 160

act ttg gtc gat ctt cac act atc cct gtg att caa tac tta ctt gga 750  
 Thr Leu Val Asp Leu His Thr Ile Pro Val Ile Gln Tyr Leu Leu Gly  
 165 170 175

act cca act aag aaa ctc ttc gac gag cgt cca cat gtg agt gct tgg 798  
 Thr Pro Thr Lys Lys Leu Phe Asp Glu Arg Pro His Val Ser Ala Trp  
 180 185 190

gtt gct gac atc act tca agg cct tct gct cag aag gtt ctt taa 843  
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&lt;210&gt; 100

&lt;211&gt; 208

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 100

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 His Val Glu Leu Lys Asp Gly Glu His Lys Lys Glu Pro Phe Ile Leu  
                   35                                  40                                  45  
 Arg Asn Pro Phe Gly Lys Val Pro Ala Phe Glu Asp Gly Asp Phe Lys  
                   50                                  55                                  60  
 Ile Phe Glu Ser Arg Ala Ile Thr Gln Tyr Ile Ala His Glu Phe Ser  
                   65                                  70                                  75                                  80  
 Asp Lys Gly Asn Asn Leu Leu Ser Thr Gly Lys Asp Met Ala Ile Ile  
                                   85                                  90                                  95  
 Ala Met Gly Ile Glu Ile Glu Ser His Glu Phe Asp Pro Val Gly Ser  
                                   100                                  105                                  110  
 Lys Leu Val Trp Glu Gln Val Leu Lys Pro Leu Tyr Gly Met Thr Thr  
                   115                                  120                                  125  
 Asp Lys Thr Val Val Glu Glu Glu Glu Ala Lys Leu Ala Lys Val Leu  
                   130                                  135                                  140  
 Asp Val Tyr Glu His Arg Leu Gly Glu Ser Lys Tyr Leu Ala Ser Asp  
                   145                                  150                                  155                                  160  
 His Phe Thr Leu Val Asp Leu His Thr Ile Pro Val Ile Gln Tyr Leu  
                                   165                                  170                                  175  
 Leu Gly Thr Pro Thr Lys Lys Leu Phe Asp Glu Arg Pro His Val Ser  
                   180                                  185                                  190  
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 Thr Ala Gly Lys Ala Gl  
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cttaaactgg aaaaattggt gaagctataa ctctttgaaa acagttgaaa cttgatcatt 157  
 actagaaatt tcagttactt gtttaattta gtttgctgta attatgtaat tgatgatttt 217  
 atgggtacaa tgggtgtcat gta g gag aag agc aat gtt ctg ctg gac aag 268  
 u Glu Lys Ser Asn Val Leu Leu Asp Lys  
 20 25

gcc aag gat gct gca gct ggt gct gga gct gga gca caa ca ggtaaacaat 319  
 Ala Lys Asp Ala Ala Ala Gly Ala Gly Ala Gly Ala Gln Gl  
 30 35 40

ccatacacag acacataaca tataatatgt aacgaaataa acgtctttgt aagcttacat 379  
 gtacgcagat ttctgatatg gttatgtata tggtata g gcg gga aag agt gta 432  
 n Ala Gly Lys Ser Val  
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tcg gat gcg gca gcg gga ggt gtt aac ttc gtg aag gac aag acc ggc 480  
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ctg aac aag tag agattcgggt caaatttggg 512  
 Leu Asn Lys  
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Asn Lys  
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 Glu Gly Lys His Tyr Phe Ser Met Trp Gln Thr Leu Phe Glu Ile Asp  
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act aag tac atg cct atc aag cct att ggt cgt gga gct tac ggt gtt 145  
 Thr Lys Tyr Met Pro Ile Lys Pro Ile Gly Arg Gly Ala Tyr Gly Val  
 30 35 40 45

gtc tgc tcc tct gtt aac agt gac acc aac gag aaa gtt gct atc aag 193  
 Val Cys Ser Ser Val Asn Ser Asp Thr Asn Glu Lys Val Ala Ile Lys  
 50 55 60

aag att cac aat gtt tat gag aat agg atc gat gcg ttg agg act ctt 241  
 Lys Ile His Asn Val Tyr Glu Asn Arg Ile Asp Ala Leu Arg Thr Leu  
 65 70 75

cgg gag ctc aag ctt cta cgc cat ctt cga cat gag aat gtc att gct 289  
 Arg Glu Leu Lys Leu Leu Arg His Leu Arg His Glu Asn Val Ile Ala  
 80 85 90

ttg aaa gat gtc atg atg cca att cat aag atg agc ttc aag gat gtt 337  
 Leu Lys Asp Val Met Met Pro Ile His Lys Met Ser Phe Lys Asp Val  
 95 100 105

tat ctt gtt tat gag ctc atg gac act gat ctc cac cag att atc aag 385  
 Tyr Leu Val Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Lys  
 110 115 120 125

tct tct cag cgt ctt agt aac gat cat tgc caa tac ttc ttg ttc cag 433  
 Ser Ser Gln Arg Leu Ser Asn Asp His Cys Gln Tyr Phe Leu Phe Gln  
 130 135 140

ttg ctt cga ggg ctc aag tat att cat tca gcc aat atc ctg cac cga 481  
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 145 150 155

gat ttg aaa cct ggt aac ctt ctt gtc aac gca aac tgc gat tta aag 529  
 Asp Leu Lys Pro Gly Asn Leu Leu Val Asn Ala Asn Cys Asp Leu Lys  
 160 165 170

ata tgc gat ttt gga cta gcg cgt gcg agc aac acc aag ggt cag ttc 577  
 Ile Cys Asp Phe Gly Leu Ala Arg Ala Ser Asn Thr Lys Gly Gln Phe  
 175 180 185

atg act gaa tat gtt gtg act cgt tgg tac cga gcc cca gag ctt ctc 625  
 Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu  
 190 195 200 205  
 ctc tgt tgt gac aac tat gga aca tcc att gat gtt tgg tct gtt ggt 673  
 Leu Cys Cys Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly  
 210 215 220  
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 Cys Ile Phe Ala Glu Leu Leu Gly Arg Lys Pro Ile Phe Gln Gly Thr  
 225 230 235  
 gaa tgt ctt aac cag ctt aag ctc att gtc aac att atc gga agc caa 769  
 Glu Cys Leu Asn Gln Leu Lys Leu Ile Val Asn Ile Ile Gly Ser Gln  
 240 245 250  
 aga gaa gaa gat ctt gag ttc ata gtt aac ccg aaa gct aaa aga tac 817  
 Arg Glu Glu Asp Leu Glu Phe Ile Val Asn Pro Lys Ala Lys Arg Tyr  
 255 260 265  
 att aga tca ctt ccg tac tca cct ggg atg tct tta tcc aga ctt tac 865  
 Ile Arg Ser Leu Pro Tyr Ser Pro Gly Met Ser Leu Ser Arg Leu Tyr  
 270 275 280 285  
 ccg tgc gct cat gta ttg gcc atc gac ctt ctg cag aaa atg ctt gtt 913  
 Pro Cys Ala His Val Leu Ala Ile Asp Leu Leu Gln Lys Met Leu Val  
 290 295 300  
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 305 310 315  
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 Tyr Met Ala Pro Leu Tyr Asp Pro Asn Ala Asn Pro Pro Ala Gln Val  
 320 325 330  
 cct atc gat ctc gat gta gat gag gat ttg aga gag gag atg ata aga 1057  
 Pro Ile Asp Leu Asp Val Asp Glu Asp Leu Arg Glu Glu Met Ile Arg  
 335 340 345  
 gaa atg ata tgg aat gag atg ctt cac tac cat cca caa gct tca acc 1105  
 Glu Met Ile Trp Asn Glu Met Leu His Tyr His Pro Gln Ala Ser Thr  
 350 355 360 365  
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&lt;210&gt; 104

&lt;211&gt; 370

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 104

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Ser	Val	Asn	Ser	Asp	Thr	Asn	Glu	Lys	Val	Ala	Ile	Lys	Lys	Ile	His
	50					55					60				
Asn	Val	Tyr	Glu	Asn	Arg	Ile	Asp	Ala	Leu	Arg	Thr	Leu	Arg	Glu	Leu
65					70					75					80
Lys	Leu	Leu	Arg	His	Leu	Arg	His	Glu	Asn	Val	Ile	Ala	Leu	Lys	Asp
				85					90					95	
Val	Met	Met	Pro	Ile	His	Lys	Met	Ser	Phe	Lys	Asp	Val	Tyr	Leu	Val
			100					105					110		
Tyr	Glu	Leu	Met	Asp	Thr	Asp	Leu	His	Gln	Ile	Ile	Lys	Ser	Ser	Gln
		115					120					125			
Arg	Leu	Ser	Asn	Asp	His	Cys	Gln	Tyr	Phe	Leu	Phe	Gln	Leu	Leu	Arg
	130					135					140				
Gly	Leu	Lys	Tyr	Ile	His	Ser	Ala	Asn	Ile	Leu	His	Arg	Asp	Leu	Lys
145					150					155					160
Pro	Gly	Asn	Leu	Leu	Val	Asn	Ala	Asn	Cys	Asp	Leu	Lys	Ile	Cys	Asp
			165					170					175		
Phe	Gly	Leu	Ala	Arg	Ala	Ser	Asn	Thr	Lys	Gly	Gln	Phe	Met	Thr	Glu
			180					185					190		
Tyr	Val	Val	Thr	Arg	Trp	Tyr	Arg	Ala	Pro	Glu	Leu	Leu	Leu	Cys	Cys
		195					200					205			
Asp	Asn	Tyr	Gly	Thr	Ser	Ile	Asp	Val	Trp	Ser	Val	Gly	Cys	Ile	Phe
	210					215					220				
Ala	Glu	Leu	Leu	Gly	Arg	Lys	Pro	Ile	Phe	Gln	Gly	Thr	Glu	Cys	Leu
225					230					235					240
Asn	Gln	Leu	Lys	Leu	Ile	Val	Asn	Ile	Ile	Gly	Ser	Gln	Arg	Glu	Glu
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Asp	Leu	Glu	Phe	Ile	Val	Asn	Pro	Lys	Ala	Lys	Arg	Tyr	Ile	Arg	Ser
			260					265					270		
Leu	Pro	Tyr	Ser	Pro	Gly	Met	Ser	Leu	Ser	Arg	Leu	Tyr	Pro	Cys	Ala
		275					280					285			
His	Val	Leu	Ala	Ile	Asp	Leu	Leu	Gln	Lys	Met	Leu	Val	Phe	Asp	Pro
	290					295					300				
Ser	Lys	Arg	Ile	Ser	Ala	Ser	Glu	Ala	Leu	Gln	His	Pro	Tyr	Met	Ala



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tgtgtagctt tttat 445

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 35 40 45

Lys Thr Arg Val Ser Ala His Gly Arg Val Gly Ala Thr Ala Ala Val  
 50 55 60

Tyr Thr Ala Ser Ile Leu Glu Tyr Leu Thr Ala Glu Val Leu Glu Leu  
 65 70 75 80

Ala Gly Asn Ala Ser Lys Asp Leu Lys Val Lys Arg Ile Thr Pro Arg  
 85 90 95

His Leu Gln Leu Ala Ile Arg Gly Asp Glu Glu Leu Asp Thr Leu Ile  
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Lys Gly Thr Ile Ala Gly Gly Gly Val Ile Pro His Ile His Lys Ser  
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Leu Ile Asn Lys Thr Thr Lys Glu  
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tat gat cca ttg cat cag aag atg tac aca ttg aat cta cct gag ctt	97
Tyr Asp Pro Leu His Gln Lys Met Tyr Thr Leu Asn Leu Pro Glu Leu	
15 20 25	
gcc aaa tct acg gtt tgt tac tca aga gat gga tgg tta cta atg cgt	145
Ala Lys Ser Thr Val Cys Tyr Ser Arg Asp Gly Trp Leu Leu Met Arg	
30 35 40	
aaa acc att tca aga gaa atg ttc ttc ttc aac ccg ttt act cgt gag	193
Lys Thr Ile Ser Arg Glu Met Phe Phe Phe Asn Pro Phe Thr Arg Glu	
45 50 55 60	
ctc ata aac gta cca aaa tgt act tta tca tat gat gcg atc gct ttc	241
Leu Ile Asn Val Pro Lys Cys Thr Leu Ser Tyr Asp Ala Ile Ala Phe	
65 70 75	
tct tgt gca cct aca tca ggt act tgc gtg ttg cta gca ttt aag cat	289
Ser Cys Ala Pro Thr Ser Gly Thr Cys Val Leu Leu Ala Phe Lys His	
80 85 90	
gtt tcg tat cgt atc acc act acg agc act tgc cat ccc aaa gca acc	337
Val Ser Tyr Arg Ile Thr Thr Thr Ser Thr Cys His Pro Lys Ala Thr	
95 100 105	
gag tgg gtt act gag gat cta caa ttc cat cgt cgc ttc cgc agt gaa	385
Glu Trp Val Thr Glu Asp Leu Gln Phe His Arg Arg Phe Arg Ser Glu	
110 115 120	
aca ctt aac cac agc aat gtt gtc tat gcc aaa cgt cgc ttc tat tgc	433
Thr Leu Asn His Ser Asn Val Val Tyr Ala Lys Arg Arg Phe Tyr Cys	
125 130 135 140	
ctt gac ggt caa gga agc tta tat tac ttt gat ccg tct tct cga aga	481
Leu Asp Gly Gln Gly Ser Leu Tyr Tyr Phe Asp Pro Ser Ser Arg Arg	
145 150 155	
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Trp Asp Phe Ser Tyr Thr Tyr Leu Leu Pro Cys Pro Tyr Ile Ser Asp	
160 165 170	
aga ttt agt tac cag tat gag cgg aag aag aag aga att ttc ttg gct	577
Arg Phe Ser Tyr Gln Tyr Glu Arg Lys Lys Lys Arg Ile Phe Leu Ala	
175 180 185	
gtg cgg aaa gga gtg ttc ttt aag ata ttt aca tgt gat ggt gag aag	625
Val Arg Lys Gly Val Phe Phe Lys Ile Phe Thr Cys Asp Gly Glu Lys	
190 195 200	
ccg ata gtg cat aag tta gaa gat atc aat tgg gag gag atc aat agt	673
Pro Ile Val His Lys Leu Glu Asp Ile Asn Trp Glu Glu Ile Asn Ser	
205 210 215 220	
act acg att gat gga ttg aca atc ttt acg ggt ctt tat tcc tct gag	721
Thr Thr Ile Asp Gly Leu Thr Ile Phe Thr Gly Leu Tyr Ser Ser Glu	
225 230 235	
gtg aga ctt aat cta cca tgg atg agg aat agt gtt tac ttt cct aga	769

Val Arg Leu Asn Leu Pro Trp Met Arg Asn Ser Val Tyr Phe Pro Arg  
 240 245 250  
 ctt cgt ttt aat gtc aag cgt tgt gta tca tat tcg ctt gat gaa gag 817  
 Leu Arg Phe Asn Val Lys Arg Cys Val Ser Tyr Ser Leu Asp Glu Glu  
 255 260 265  
 agg tat tat ccg cgg aag cag tgg caa gaa cag gag gat tta tgt cct 865  
 Arg Tyr Tyr Pro Arg Lys Gln Trp Gln Glu Gln Glu Asp Leu Cys Pro  
 270 275 280  
 att gag aat ctt tgg att agg cca ccg aag aaa gct gta gat ttc atg 913  
 Ile Glu Asn Leu Trp Ile Arg Pro Pro Lys Lys Ala Val Asp Phe Met  
 285 290 295 300  
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&lt;210&gt; 108

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 108

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 Arg Glu Met Phe Phe Phe Asn Pro Phe Thr Arg Glu Leu Ile Asn Val  
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 Pro Lys Cys Thr Leu Ser Tyr Asp Ala Ile Ala Phe Ser Cys Ala Pro  
 65 70 75 80  
 Thr Ser Gly Thr Cys Val Leu Leu Ala Phe Lys His Val Ser Tyr Arg  
 85 90 95  
 Ile Thr Thr Thr Ser Thr Cys His Pro Lys Ala Thr Glu Trp Val Thr  
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 Glu Asp Leu Gln Phe His Arg Arg Phe Arg Ser Glu Thr Leu Asn His  
 115 120 125  
 Ser Asn Val Val Tyr Ala Lys Arg Arg Phe Tyr Cys Leu Asp Gly Gln  
 130 135 140  
 Gly Ser Leu Tyr Tyr Phe Asp Pro Ser Ser Arg Arg Trp Asp Phe Ser  
 145 150 155 160  
 Tyr Thr Tyr Leu Leu Pro Cys Pro Tyr Ile Ser Asp Arg Phe Ser Tyr  
 165 170 175

Gln Tyr Glu Arg Lys Lys Lys Arg Ile Phe Leu Ala Val Arg Lys Gly  
 180 185 190  
 Val Phe Phe Lys Ile Phe Thr Cys Asp Gly Glu Lys Pro Ile Val His  
 195 200 205  
 Lys Leu Glu Asp Ile Asn Trp Glu Glu Ile Asn Ser Thr Thr Ile Asp  
 210 215 220  
 Gly Leu Thr Ile Phe Thr Gly Leu Tyr Ser Ser Glu Val Arg Leu Asn  
 225 230 235 240  
 Leu Pro Trp Met Arg Asn Ser Val Tyr Phe Pro Arg Leu Arg Phe Asn  
 245 250 255  
 Val Lys Arg Cys Val Ser Tyr Ser Leu Asp Glu Glu Arg Tyr Tyr Pro  
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gatacctaaa ccaaattccaa ttca atg gcg gaa gaa gca aaa tcc aaa gga	171
Met Ala Glu Glu Ala Lys Ser Lys Gly	
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aac gca gct ttc tct tcc ggc gat tac gcc acc gca ata acc cat ttc	219
Asn Ala Ala Phe Ser Ser Gly Asp Tyr Ala Thr Ala Ile Thr His Phe	
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aca gaa gca atc aac ctt tca cca acc aat cac atc ctc tac tca aac	267
Thr Glu Ala Ile Asn Leu Ser Pro Thr Asn His Ile Leu Tyr Ser Asn	
30 35 40	
aga tcc gct tct tac gct tct ctc cac cgt tac gaa gaa gct tta tca	315
Arg Ser Ala Ser Tyr Ala Ser Leu His Arg Tyr Glu Glu Ala Leu Ser	
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gac gcg aag aag act ata gag ctt aaa cct gat tgg tct aaa gga tat	363
Asp Ala Lys Lys Thr Ile Glu Leu Lys Pro Asp Trp Ser Lys Gly Tyr	
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Ser Arg Leu Gly Ala Ala Phe Ile Gly Leu Ser Lys Phe Asp Glu Ala	
75 80 85	
gtt gat tcg tat aag aaa gga tta gag att gat ccg agt aat gag atg	459
Val Asp Ser Tyr Lys Lys Gly Leu Glu Ile Asp Pro Ser Asn Glu Met	
90 95 100 105	
ctt aaa tcg gga tta gct gat gct tcg aga tct agg gtt tcg tca aag	507
Leu Lys Ser Gly Leu Ala Asp Ala Ser Arg Ser Arg Val Ser Ser Lys	
110 115 120	
tcg aat cct ttt gtt gat gcg ttt caa ggg aag gag atg tgg gag aag	555
Ser Asn Pro Phe Val Asp Ala Phe Gln Gly Lys Glu Met Trp Glu Lys	
125 130 135	
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Leu Thr Ala Asp Pro Gly Thr Arg Val Tyr Leu Glu Gln Asp Asp Phe	
140 145 150	
gtt aag acg atg aag gag att cag agg aac cct aat aat ctt aat ttg	651
Val Lys Thr Met Lys Glu Ile Gln Arg Asn Pro Asn Asn Leu Asn Leu	
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Tyr Met Lys Asp Lys Arg Val Met Lys Ala Leu Gly Val Leu Leu Asn	
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Val Lys Phe Gly Gly Ser Ser Gly Glu Asp Thr Glu Met Lys Glu Ala	
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gat gag agg aaa gag cct gaa ccg gag atg gaa cct atg gag ttg acg	795
Asp Glu Arg Lys Glu Pro Glu Pro Glu Met Glu Pro Met Glu Leu Thr	
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gag gag gag agg cag aag aag gag aga aag gag aag gct ttg aag gag	843

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 Val Glu His Tyr Thr Lys Ala Met Glu Leu Asp Asp Glu Asp Ile Ser  
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 Tyr Leu Thr Asn Arg Ala Ala Val Tyr Leu Glu Met Gly Lys  
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 Asp Ala Glu Lys Val Lys Lys Glu Leu Glu Gln Gln Glu Tyr Phe Asp  
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 Pro Thr Ile Ala Glu Glu Glu Arg Glu Lys G  
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 aag cat tat tca gaa gca atc aaa aga aac ccg aac gac gtg agg gca 1905  
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 390 395 400 405  
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 Tyr Ser Asn Arg Ala Ala Cys Tyr Thr Lys Leu Gly Ala Leu Pro Glu  
 410 415 420  
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 Gly Leu Lys Asp Ala Glu Lys Cys Ile Glu Leu Asp Pro Ser Phe Thr  
 425 430 435  
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 Lys Gly Tyr Ser Arg Lys Gly Ala Ile Gln Phe Phe Met Lys Glu Tyr  
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 Asp Lys Ala Met Glu Thr Tyr Gln Glu Gly Leu Lys His Asp Pro Lys  
 455 460 465  
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 Asn Gln Glu Phe Leu Asp Gly Val Arg Ar  
 470 475  
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 Cys Val Glu Gln Ile Asn Lys Ala Ser Arg Gly Asp Leu Thr Pro Glu  
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 Glu Leu Lys Glu Arg Gln Ala Lys Ala Met Gln Asp Pro Glu Val Gln  
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 aac ata tta tcg gat cca gtg atg aga cag gtaaaagcag tggcaagcat 2350  
 Asn Ile Leu Ser Asp Pro Val Met Arg Gln  
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 Val  
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 Leu Val Asp Phe Gln Glu Asn Pro Lys Ala Ala Gln Glu His Met Lys  
 525 530 535  
 aac cca atg gta atg aac aag att cag aag ctg gtt agt gcc gga att 2503  
 Asn Pro Met Val Met Asn Lys Ile Gln Lys Leu Val Ser Ala Gly Ile  
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 gtt cag gtc cgg taa attgggttatg ctaaaccgga gtgggtatatt gaatcaaacc 2558



Val Gln Val Arg  
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Leu His Arg Tyr Glu Glu Ala Leu Ser Asp Ala Lys Lys Thr Ile Glu  
50 55 60  
Leu Lys Pro Asp Trp Ser Lys Gly Tyr Ser Arg Leu Gly Ala Ala Phe  
65 70 75 80  
Ile Gly Leu Ser Lys Phe Asp Glu Ala Val Asp Ser Tyr Lys Lys Gly  
85 90 95  
Leu Glu Ile Asp Pro Ser Asn Glu Met Leu Lys Ser Gly Leu Ala Asp  
100 105 110  
Ala Ser Arg Ser Arg Val Ser Ser Lys Ser Asn Pro Phe Val Asp Ala  
115 120 125  
Phe Gln Gly Lys Glu Met Trp Glu Lys Leu Thr Ala Asp Pro Gly Thr  
130 135 140  
Arg Val Tyr Leu Glu Gln Asp Asp Phe Val Lys Thr Met Lys Glu Ile  
145 150 155 160  
Gln Arg Asn Pro Asn Asn Leu Asn Leu Tyr Met Lys Asp Lys Arg Val  
165 170 175  
Met Lys Ala Leu Gly Val Leu Leu Asn Val Lys Phe Gly Gly Ser Ser  
180 185 190  
Gly Glu Asp Thr Glu Met Lys Glu Ala Asp Glu Arg Lys Glu Pro Glu  
195 200 205  
Pro Glu Met Glu Pro Met Glu Leu Thr Glu Glu Glu Arg Gln Lys Lys  
210 215 220  
Glu Arg Lys Glu Lys Ala Leu Lys Glu Lys Gly Glu Gly Asn Val Ala

225		230		235		240
Tyr Lys Lys Lys Asp Phe Gly Arg Ala Val Glu His Tyr Thr Lys Ala	245			250		255
Met Glu Leu Asp Asp Glu Asp Ile Ser Tyr Leu Thr Asn Arg Ala Ala	260		265			270
Val Tyr Leu Glu Met Gly Lys Tyr Glu Glu Cys Ile Glu Asp Cys Asp	275		280		285	
Lys Ala Val Glu Arg Gly Arg Glu Leu Arg Ser Asp Phe Lys Met Ile	290		295		300	
Ala Arg Ala Leu Thr Arg Lys Gly Ser Ala Leu Val Lys Met Ala Arg	305		310		315	320
Cys Ser Lys Asp Phe Glu Pro Ala Ile Glu Thr Phe Gln Lys Ala Leu	325		330			335
Thr Glu His Arg Asn Pro Asp Thr Leu Lys Lys Leu Asn Asp Ala Glu	340		345			350
Lys Val Lys Lys Glu Leu Glu Gln Gln Glu Tyr Phe Asp Pro Thr Ile	355		360		365	
Ala Glu Glu Glu Arg Glu Lys Gly Asn Gly Phe Phe Lys Glu Gln Lys	370		375		380	
Tyr Pro Glu Ala Val Lys His Tyr Ser Glu Ala Ile Lys Arg Asn Pro	385		390		395	400
Asn Asp Val Arg Ala Tyr Ser Asn Arg Ala Ala Cys Tyr Thr Lys Leu	405		410			415
Gly Ala Leu Pro Glu Gly Leu Lys Asp Ala Glu Lys Cys Ile Glu Leu	420		425			430
Asp Pro Ser Phe Thr Lys Gly Tyr Ser Arg Lys Gly Ala Ile Gln Phe	435		440		445	
Phe Met Lys Glu Tyr Asp Lys Ala Met Glu Thr Tyr Gln Glu Gly Leu	450		455		460	
Lys His Asp Pro Lys Asn Gln Glu Phe Leu Asp Gly Val Arg Arg Cys	465		470		475	480
Val Glu Gln Ile Asn Lys Ala Ser Arg Gly Asp Leu Thr Pro Glu Glu	485		490			495
Leu Lys Glu Arg Gln Ala Lys Ala Met Gln Asp Pro Glu Val Gln Asn	500		505			510
Ile Leu Ser Asp Pro Val Met Arg Gln Val Leu Val Asp Phe Gln Glu	515		520		525	
Asn Pro Lys Ala Ala Gln Glu His Met Lys Asn Pro Met Val Met Asn						

530

535

540

Lys Ile Gln Lys Leu Val Ser Ala Gly Ile Val Gln Val Arg  
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&lt;211&gt; 1560

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&lt;222&gt; (386)..(515)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (622)..(1480)

&lt;400&gt; 111

tatataaacc tcacacacgc attatcatatc accatcctcc tcattctctt catcatcaac 60

ataagagaga gagaagaaaa aaagaattac aattaataag aacaagatca agaatacaaga 120

atcaagaaa atg gga aga gca ccg tgt tgt gat aag gcc aac gtg aag aaa 171

Met Gly Arg Ala Pro Cys Cys Asp Lys Ala Asn Val Lys Lys

1

5

10

ggg cct tgg tct cct gag gaa gac gcc aaa ctc aaa gat tac atc gag 219

Gly Pro Trp Ser Pro Glu Glu Asp Ala Lys Leu Lys Asp Tyr Ile Glu

15

20

25

30

aat agt ggc aca gga ggc aac tgg att gct ttg cct cag aaa att g 265

Asn Ser Gly Thr Gly Gly Asn Trp Ile Ala Leu Pro Gln Lys Ile G

35

40

45

gtatgtatta cttaaaactc acttttgatt taaaattggc actgagagtt tccaaatagt 325

actttgagac cgtggtcgtg ttaaatttgt gtgttgatga tatttattta catggtatag 385

gt tta agg aga tgt ggg aag agt tgc agg cta agg tgg ctc aac tat 432

ly Leu Arg Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr

50

55

60

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Leu Arg Pro Asn Ile Lys His Gly Gly Phe Ser Glu Glu Glu Asp Asn

65

70

75

atc att tgt aac ctc tat gtt act att ggt agc ag gtactatata 525

Ile Ile Cys Asn Leu Tyr Val Thr Ile Gly Ser Ar

80

85

cttacatata tatcatcata tgcattgatg aatattatta attgacacac ttattcttga 585

cttagagact cactatgtat ctttgtttaa ttctag g tgg tct ata att gct gca 640  
g Trp Ser Ile Ile Ala Ala  
90 95

caa ttg ccg gga aga acc gac aac gat atc aaa aac tat tgg aac acg 688  
Gln Leu Pro Gly Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr  
100 105 110

agg ctg aag aag aag ctt ctg aac aaa caa agg aaa gag ttc caa gaa 736  
Arg Leu Lys Lys Lys Leu Leu Asn Lys Gln Arg Lys Glu Phe Gln Glu  
115 120 125

gcg cga atg aag caa gag atg gtg atg atg aaa agg caa caa caa gga 784  
Ala Arg Met Lys Gln Glu Met Val Met Met Lys Arg Gln Gln Gln Gly  
130 135 140

caa gga caa ggt caa agt aat ggt agt acg gat ctt tat ctt aac aac 832  
Gln Gly Gln Gly Gln Ser Asn Gly Ser Thr Asp Leu Tyr Leu Asn Asn  
145 150 155

atg ttt gga tca tca cca tgg cca tta cta cca caa ctt cct cct cca 880  
Met Phe Gly Ser Ser Pro Trp Pro Leu Leu Pro Gln Leu Pro Pro Pro  
160 165 170 175

cat cat caa ata cct ctt gga atg atg gaa cca aca agc tgt aac tac 928  
His His Gln Ile Pro Leu Gly Met Met Glu Pro Thr Ser Cys Asn Tyr  
180 185 190

tac caa acg aca ccg tct tgt aac cta gaa caa aag cca ttg atc aca 976  
Tyr Gln Thr Thr Pro Ser Cys Asn Leu Glu Gln Lys Pro Leu Ile Thr  
195 200 205

ctc aag aac atg gtc aag att gaa gaa gaa cag gaa agg aca aac cct 1024  
Leu Lys Asn Met Val Lys Ile Glu Glu Glu Gln Glu Arg Thr Asn Pro  
210 215 220

gat cat cat cat caa gat tct gtc aca aac cct ttt gat ttc tct ttc 1072  
Asp His His His Gln Asp Ser Val Thr Asn Pro Phe Asp Phe Ser Phe  
225 230 235

tct cag ctt ttg tta gat ccc aat tac tat ctg gga tca gga ggg gga 1120  
Ser Gln Leu Leu Leu Asp Pro Asn Tyr Tyr Leu Gly Ser Gly Gly Gly  
240 245 250 255

gga gaa gga gat ttt gct atc atg agc agc agc aca aac tca cca tta 1168  
Gly Glu Gly Asp Phe Ala Ile Met Ser Ser Ser Thr Asn Ser Pro Leu  
260 265 270

cca aac aca agt agt gat caa cat cca agt caa cag caa gag att ctt 1216  
Pro Asn Thr Ser Ser Asp Gln His Pro Ser Gln Gln Gln Glu Ile Leu  
275 280 285

caa tgg ttt ggg agc agt aac ttt cag aca gaa gca atc aac gat atg 1264  
Gln Trp Phe Gly Ser Ser Asn Phe Gln Thr Glu Ala Ile Asn Asp Met  
290 295 300

ttc ata aac aac aac aac aac ata gtg aat ctt gag acc atc gag aac 1312  
 Phe Ile Asn Asn Asn Asn Asn Ile Val Asn Leu Glu Thr Ile Glu Asn  
 305 310 315

aca aaa gtc tat gga gac gcc tca gta gcc gga gcc gct gtc cga gca 1360  
 Thr Lys Val Tyr Gly Asp Ala Ser Val Ala Gly Ala Ala Val Arg Ala  
 320 325 330 335

gct ttg ggc gga ggg aca acg agt aca tcg gcg gat caa agt aca ata 1408  
 Ala Leu Gly Gly Gly Thr Thr Ser Thr Ser Ala Asp Gln Ser Thr Ile  
 340 345 350

agt tgg gag gat ata act tct cta gtt aat tcc gaa gat gca agt tac 1456  
 Ser Trp Glu Asp Ile Thr Ser Leu Val Asn Ser Glu Asp Ala Ser Tyr  
 355 360 365

ttc aat gcg cca aat cat gtg taa cattttgttt aaaactttat ttgtacttaa 1510  
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<212> PRT

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Gly Thr Gly Gly Asn Trp Ile Ala Leu Pro Gln Lys Ile Gly Leu Arg  
 35 40 45

Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro  
 50 55 60

Asn Ile Lys His Gly Gly Phe Ser Glu Glu Glu Asp Asn Ile Ile Cys  
 65 70 75 80

Asn Leu Tyr Val Thr Ile Gly Ser Arg Trp Ser Ile Ile Ala Ala Gln  
 85 90 95

Leu Pro Gly Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr Arg  
 100 105 110

Leu Lys Lys Lys Leu Leu Asn Lys Gln Arg Lys Glu Phe Gln Glu Ala  
 115 120 125

Arg Met Lys Gln Glu Met Val Met Met Lys Arg Gln Gln Gln Gly Gln  
 130 135 140

Gly Gln Gly Gln Ser Asn Gly Ser Thr Asp Leu Tyr Leu Asn Asn Met  
 145 150 155 160  
 Phe Gly Ser Ser Pro Trp Pro Leu Leu Pro Gln Leu Pro Pro Pro His  
 165 170 175  
 His Gln Ile Pro Leu Gly Met Met Glu Pro Thr Ser Cys Asn Tyr Tyr  
 180 185 190  
 Gln Thr Thr Pro Ser Cys Asn Leu Glu Gln Lys Pro Leu Ile Thr Leu  
 195 200 205  
 Lys Asn Met Val Lys Ile Glu Glu Gln Glu Arg Thr Asn Pro Asp  
 210 215 220  
 His His His Gln Asp Ser Val Thr Asn Pro Phe Asp Phe Ser Phe Ser  
 225 230 235 240  
 Gln Leu Leu Leu Asp Pro Asn Tyr Tyr Leu Gly Ser Gly Gly Gly Gly  
 245 250 255  
 Glu Gly Asp Phe Ala Ile Met Ser Ser Ser Thr Asn Ser Pro Leu Pro  
 260 265 270  
 Asn Thr Ser Ser Asp Gln His Pro Ser Gln Gln Gln Glu Ile Leu Gln  
 275 280 285  
 Trp Phe Gly Ser Ser Asn Phe Gln Thr Glu Ala Ile Asn Asp Met Phe  
 290 295 300  
 Ile Asn Asn Asn Asn Asn Ile Val Asn Leu Glu Thr Ile Glu Asn Thr  
 305 310 315 320  
 Lys Val Tyr Gly Asp Ala Ser Val Ala Gly Ala Ala Val Arg Ala Ala  
 325 330 335  
 Leu Gly Gly Gly Thr Thr Ser Thr Ser Ala Asp Gln Ser Thr Ile Ser  
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Gly Ser Ser Val Ala Lys Leu Ala Ile Arg Arg Thr Leu Ser Gln Ser  
10 15 20

cgt tgt ggt tca tat gcc act aga aca agg gtt ttg cct tgt caa acc 151  
Arg Cys Gly Ser Tyr Ala Thr Arg Thr Arg Val Leu Pro Cys Gln Thr  
25 30 35

aga tgt ttt cac tct aca ata ctc aaa tca aag gca gag tct gct gca 199  
Arg Cys Phe His Ser Thr Ile Leu Lys Ser Lys Ala Glu Ser Ala Ala  
40 45 50

cct gtt cca cgt cct gtc cca ctt tct aag cta act gat agc ttc tta 247  
Pro Val Pro Arg Pro Val Pro Leu Ser Lys Leu Thr Asp Ser Phe Leu  
55 60 65 70

gat gga aca agc agt gtg tat cta gag gag tta caa aga gct tgg gag 295  
Asp Gly Thr Ser Ser Val Tyr Leu Glu Glu Leu Gln Arg Ala Trp Glu  
75 80 85

gct gat ccc aac agt gtt gat gag tcg tgg gat aac ttt ttt agg aat 343  
Ala Asp Pro Asn Ser Val Asp Glu Ser Trp Asp Asn Phe Phe Arg Asn  
90 95 100

ttt gtg ggt cag gct tct aca tcg cct ggt atc tcg ggg caa acc att 391  
Phe Val Gly Gln Ala Ser Thr Ser Pro Gly Ile Ser Gly Gln Thr Ile  
105 110 115

caa gaa agc atg cgt ttg ttg ttg cta gtt aga gct tac cag gtt aat 439

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Ile Arg Arg Thr Leu Thr Lys Pro His Gly Thr Phe Ser Arg Cys Arg
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Tyr Leu Ser Thr Ala Ala Ala Thr Glu Val Asn Tyr Glu Asp Glu
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tcg att atg atg aaa gga gtt cga att tca ggt aga cct ctt tac tta 195
Ser Ile Met Met Lys Gly Val Arg Ile Ser Gly Arg Pro Leu Tyr Leu
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gat atg caa gcg acg act ccg att gat cct aga gta ttc gat gcg atg 243
Asp Met Gln Ala Thr Thr Pro Ile Asp Pro Arg Val Phe Asp Ala Met
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Asn Ala Ser Gln Ile His Glu Tyr Gly Asn Pro His Ser Arg Thr His
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ctc tac ggc tgg gaa gct gag aac gcc gtc gag aac gca cga aac cag 339
Leu Tyr Gly Trp Glu Ala Glu Asn Ala Val Glu Asn Ala Arg Asn Gln
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gtc gcg aaa ctg atc gaa gct tca ccg aag gag atc gta ttc gtg tcc 387
Val Ala Lys Leu Ile Glu Ala Ser Pro Lys Glu Ile Val Phe Val Ser
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Gly Ala Thr Glu Ala Asn Asn Met Ala Val Lys Gly Val Met His Phe
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tac aag gac acg aag aaa cat gtg ata act aca cag act gag cat aag 483
Tyr Lys Asp Thr Lys Lys His Val Ile Thr Thr Gln Thr Glu His Lys
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tgt gtg ctt gat tcg tgt agg cat ttg cag caa gaa gga ttt gag gta 531
Cys Val Leu Asp Ser Cys Arg His Leu Gln Gln Glu Gly Phe Glu Val
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act tat tta cct gtg aaa act gat gga ttg gtt gat tta gag atg ttg 579
Thr Tyr Leu Pro Val Lys Thr Asp Gly Leu Val Asp Leu Glu Met Leu
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aga gaa gct att agg cca gac aca ggg cta gtt tct att atg gct gtg 627
Arg Glu Ala Ile Arg Pro Asp Thr Gly Leu Val Ser Ile Met Ala Val
                      190                      195                      200

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Asn Asn Glu Ile Gly Val Val Gln Pro Met Glu Glu Ile Gly Met Ile
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Gly Lys Ile Pro Val Asp Val Lys Lys Trp Asn Val Ala Leu Met Ser	
235 240 245	
atg agt gct cac aag atc tat gga ccg aaa ggt gtt ggt gct ttg tat	819
Met Ser Ala His Lys Ile Tyr Gly Pro Lys Gly Val Gly Ala Leu Tyr	
250 255 260 265	
gtg agg agg agg ccg aga atc agg ctt gag ccg ttg atg aat ggt gga	867
Val Arg Arg Arg Pro Arg Ile Arg Leu Glu Pro Leu Met Asn Gly Gly	
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Gly Gln Glu Arg Gly Leu Arg Ser Gly Thr Gly Ala Thr Gln Gln Ile	
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Val Gly Phe Gly Ala Ala Cys Glu Leu Ala Met Lys Glu Met Glu Tyr	
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gat gag aag tgg att aag ggg tta cag gag agg ttg ctg aat ggg gtt	1011
Asp Glu Lys Trp Ile Lys Gly Leu Gln Glu Arg Leu Leu Asn Gly Val	
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Arg Glu Lys Leu Asp Gly Val Val Val Asn Gly Ser Met Asp Ser Arg	
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Tyr Val Gly Asn Leu Asn Leu Ser Phe Ala Tyr Val Glu Gly Glu Ser	
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Thr Ser Ala Ser Leu Glu Pro Ser Tyr Val Leu Arg Ala Leu Gly Val	
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Asp Glu Asp Met Ala His Thr Ser Ile Arg Phe Gly Ile Gly Arg Phe	
395 400 405	
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Thr Thr Lys Glu Glu Ile Asp Lys Ala Val Glu Leu Thr Val Lys Gln	
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Val Glu Lys Leu Arg Glu Met Ser Pro Leu Tyr Glu Met Val Lys Glu	
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cca

1399

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&lt;211&gt; 453

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&lt;400&gt; 118

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Tyr Gly Asn Pro His Ser Arg Thr His Leu Tyr Gly Trp Glu Ala Glu  
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100 105 110

Ser Pro Lys Glu Ile Val Phe Val Ser Gly Ala Thr Glu Ala Asn Asn  
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Met Ala Val Lys Gly Val Met His Phe Tyr Lys Asp Thr Lys Lys His  
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Val Ile Thr Thr Gln Thr Glu His Lys Cys Val Leu Asp Ser Cys Arg  
145 150 155 160

His Leu Gln Gln Glu Gly Phe Glu Val Thr Tyr Leu Pro Val Lys Thr  
165 170 175

Asp Gly Leu Val Asp Leu Glu Met Leu Arg Glu Ala Ile Arg Pro Asp  
180 185 190

Thr Gly Leu Val Ser Ile Met Ala Val Asn Asn Glu Ile Gly Val Val  
195 200 205

Gln Pro Met Glu Glu Ile Gly Met Ile Cys Lys Glu His Asn Val Pro  
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Phe His Thr Asp Ala Ala Gln Ala Ile Gly Lys Ile Pro Val Asp Val  
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Lys Lys Trp Asn Val Ala Leu Met Ser Met Ser Ala His Lys Ile Tyr  
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 Gly Pro Lys Gly Val Gly Ala Leu Tyr Val Arg Arg Arg Pro Arg Ile  
 260 265 270  
 Arg Leu Glu Pro Leu Met Asn Gly Gly Gly Gln Glu Arg Gly Leu Arg  
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 Glu Leu Ala Met Lys Glu Met Glu Tyr Asp Glu Lys Trp Ile Lys Gly  
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 Val Val Asn Gly Ser Met Asp Ser Arg Tyr Val Gly Asn Leu Asn Leu  
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 Ser Phe Ala Tyr Val Glu Gly Glu Ser Leu Leu Met Gly Leu Lys Glu  
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 Val Ala Val Ser Ser Gly Ser Ala Cys Thr Ser Ala Ser Leu Glu Pro  
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 Ser Tyr Val Leu Arg Ala Leu Gly Val Asp Glu Asp Met Ala His Thr  
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 Ser Ile Arg Phe Gly Ile Gly Arg Phe Thr Thr Lys Glu Glu Ile Asp  
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Leu Leu Ser Cys Phe Leu Gln Val Ser Ser Asn Gly Asp Ala Glu Ile	
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Leu Ser Arg Val Lys Lys Thr Arg Leu Phe Asp Pro Asp Gly Asn Leu	
35 40 45	
caa gat tgg gtc ata acc gga gat aat cgg agt cca tgt aat tgg acg	193
Gln Asp Trp Val Ile Thr Gly Asp Asn Arg Ser Pro Cys Asn Trp Thr	
50 55 60	
gga atc aca tgc cac atc aga aaa ggt agc tcc ctc gcc gtc act acc	241
Gly Ile Thr Cys His Ile Arg Lys Gly Ser Ser Leu Ala Val Thr Thr	
65 70 75	
att gat ctc tcc ggc tat aat atc tcc ggt ggc ttt ccc tac gga ttc	289
Ile Asp Leu Ser Gly Tyr Asn Ile Ser Gly Gly Phe Pro Tyr Gly Phe	
80 85 90	
tgt cgt atc cgt aca ctc atc aac atc act ctt tct caa aac aat ctc	337
Cys Arg Ile Arg Thr Leu Ile Asn Ile Thr Leu Ser Gln Asn Asn Leu	
95 100 105 110	
aat ggt acg att gat tct gct cct ctc tcc ctc tgt tct aaa ctt cag	385
Asn Gly Thr Ile Asp Ser Ala Pro Leu Ser Leu Cys Ser Lys Leu Gln	
115 120 125	
aat ttg att ctc aat caa aac aac ttc tcc ggt aaa tta ccg gaa ttc	433
Asn Leu Ile Leu Asn Gln Asn Asn Phe Ser Gly Lys Leu Pro Glu Phe	
130 135 140	
tca ccg gag ttt cgt aaa tta cga gtc ctc gaa ttg gaa tca aac ctc	481
Ser Pro Glu Phe Arg Lys Leu Arg Val Leu Glu Leu Glu Ser Asn Leu	
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ttc acc ggt gag att cct caa agt tac ggg aga ctc act gct ctg caa	529
Phe Thr Gly Glu Ile Pro Gln Ser Tyr Gly Arg Leu Thr Ala Leu Gln	
160 165 170	
gtt ctg aat ctt aat ggt aac ccg ctc agt gga atc gtt ccg gcg ttt	577
Val Leu Asn Leu Asn Gly Asn Pro Leu Ser Gly Ile Val Pro Ala Phe	
175 180 185 190	
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Leu Gly Tyr Leu Thr Glu Leu Thr Arg Leu Asp Leu Ala Tyr Ile Ser	
195 200 205	

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Phe Asp Pro Ser Pro Ile Pro Ser Thr Leu Gly Asn Leu Ser Asn Leu	
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act gat ctt cgg cta act cac tcg aac ctc gtc gga gaa att cct gat	721
Thr Asp Leu Arg Leu Thr His Ser Asn Leu Val Gly Glu Ile Pro Asp	
225 230 235	
tcg atc atg aat ctg gtg ttg tta gag aat ctt gat tta gct atg aat	769
Ser Ile Met Asn Leu Val Leu Leu Glu Asn Leu Asp Leu Ala Met Asn	
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Ser Leu Thr Gly Glu Ile Pro Glu Ser Ile Gly Arg Leu Glu Ser Val	
255 260 265 270	
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Tyr Gln Ile Glu Leu Tyr Asp Asn Arg Leu Ser Gly Lys Leu Pro Glu	
275 280 285	
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Ser Ile Gly Asn Leu Thr Glu Leu Arg Asn Phe Asp Val Ser Gln Asn	
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Asn Leu Thr Gly Glu Leu Pro Glu Lys Ile Ala Ala Leu Gln Leu Ile	
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320 325 330	
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Val Ala Leu Asn Pro Asn Leu Val Glu Phe Lys Ile Phe Asn Asn Ser	
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Phe Thr Gly Thr Leu Pro Arg Asn Leu Gly Lys Phe Ser Glu Ile Ser	
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Glu Phe Asp Val Ser Thr Asn Arg Phe Ser Gly Glu Leu Pro Pro Tyr	
370 375 380	
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Leu Cys Tyr Arg Arg Lys Leu Gln Lys Ile Ile Thr Phe Ser Asn Gln	
385 390 395	
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Leu Ser Gly Glu Ile Pro Glu Ser Tyr Gly Asp Cys His Ser Leu Asn	
400 405 410	
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Tyr Ile Arg Met Ala Asp Asn Lys Leu Ser Gly Glu Val Pro Ala Arg	
415 420 425 430	
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Phe	Trp	Glu	Leu	Pro	Leu	Thr	Arg	Leu	Glu	Leu	Ala	Asn	Asn	Asn	Gln	
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tta	caa	ggt	tcg	att	cct	cct	tcg	att	tcc	aaa	gct	cgt	cat	cta	tct	1393
Leu	Gln	Gly	Ser	Ile	Pro	Pro	Ser	Ile	Ser	Lys	Ala	Arg	His	Leu	Ser	
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cag	ctt	gaa	atc	tcc	gct	aac	aac	ttc	tcc	ggt	gtg	att	ccc	gtc	aaa	1441
Gln	Leu	Glu	Ile	Ser	Ala	Asn	Asn	Phe	Ser	Gly	Val	Ile	Pro	Val	Lys	
			465					470					475			
ctt	tgt	gat	ctc	cgt	gat	ctc	aga	gtc	atc	gat	ctt	agc	cgc	aac	agt	1489
Leu	Cys	Asp	Leu	Arg	Asp	Leu	Arg	Val	Ile	Asp	Leu	Ser	Arg	Asn	Ser	
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ttc	tta	gga	tca	att	ccg	tct	tgc	atc	aac	aaa	ttg	aag	aat	cta	gag	1537
Phe	Leu	Gly	Ser	Ile	Pro	Ser	Cys	Ile	Asn	Lys	Leu	Lys	Asn	Leu	Glu	
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Arg	Val	Glu	Met	Gln	Glu	Asn	Met	Leu	Asp	Gly	Glu	Ile	Pro	Ser	Ser	
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gtg	agt	tcg	tgc	acc	gag	tta	acc	gaa	tta	aat	ctc	tcc	aac	aac	cgt	1633
Val	Ser	Ser	Cys	Thr	Glu	Leu	Thr	Glu	Leu	Asn	Leu	Ser	Asn	Asn	Arg	
			530					535					540			
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Leu	Arg	Gly	Gly	Ile	Pro	Pro	Glu	Leu	Gly	Asp	Leu	Pro	Val	Leu	Asn	
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tac	ctg	gat	ctc	tct	aac	aac	caa	ctc	acc	ggt	gag	att	ccg	gcg	gag	1729
Tyr	Leu	Asp	Leu	Ser	Asn	Asn	Gln	Leu	Thr	Gly	Glu	Ile	Pro	Ala	Glu	
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Tyr	G							ly								
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Asn	Pro	Asn	Leu	Cys	Ala	Pro	Asn	Leu	Asp	Pro	Ile	Arg	Pro	Cys	Arg	
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Ser	Lys	Arg	Glu	Thr	Arg	Tyr	Ile	Leu	Pro	Ile	Ser	Ile	Leu	Cys	Ile	
			610				615					620				
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Val	Ala	Leu	Thr	Gly	Ala	Leu	Val	Trp	Leu	Phe	Ile	Lys	Thr	Lys	Pro	
			625			630				635					640	
tta	ttc	aag	aga	aaa	ccg	aaa	cgg	acc	aac	aaa	ata	acc	atc	ttc	cag	2026
Leu	Phe	Lys	Arg	Lys	Pro	Lys	Arg	Thr	Asn	Lys	Ile	Thr	Ile	Phe	Gln	
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Asn Ile Ile Gly Ser Gly Gly Ser Gly Leu Val Tyr Arg Val Lys Leu	
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Lys Ser Gly Gln Thr Leu Ala Val Lys Lys Leu Trp Gly Glu Thr Gly	
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Gln Lys Thr Glu Ser Glu Ser Val Phe Arg Ser Glu Val Glu Thr Leu	
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Gly Arg Val Arg His Gly Asn Ile Val Lys Leu Leu Met Cys Cys Asn	
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Gly Glu Glu Phe Arg Phe Leu Val Tyr Glu Phe Met Glu Asn Gly Ser	
740 745 750	
tta ggt gac gtt ttg cat tcg gag aaa gaa cat cgt gcc gtt tct cca	2362
Leu Gly Asp Val Leu His Ser Glu Lys Glu His Arg Ala Val Ser Pro	
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Leu Asp Trp Thr Thr Arg Phe Ser Ile Ala Val Gly Ala Ala Gln Gly	
770 775 780	
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Leu Ser Tyr Leu His His Asp Ser Val Pro Pro Ile Val His Arg Asp	
785 790 795 800	
gtc aaa agc aat aat ata ttg ttg gac cat gag atg aag cca cgt gtc	2506
Val Lys Ser Asn Asn Ile Leu Leu Asp His Glu Met Lys Pro Arg Val	
805 810 815	
gcc gat ttc ggt tta gct aaa ccg ttg aag aga gaa gac aat gat ggt	2554
Ala Asp Phe Gly Leu Ala Lys Pro Leu Lys Arg Glu Asp Asn Asp Gly	
820 825 830	
gtc tcc gat gtt tca atg tct tgt gtt gct gga tcc tac ggc tac att	2602
Val Ser Asp Val Ser Met Ser Cys Val Ala Gly Ser Tyr Gly Tyr Ile	
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Ala Pro G	
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 Lys Val Asn Glu Lys Ser Asp Val Tyr Ser Phe Gly Val Val Leu Leu  
 860 865 870  
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 Glu Leu Ile Thr Gly Lys Arg Pro Asn Asp Ser Ser Phe Gly Glu Asn  
 875 880 885  
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 Arg Asp Leu Ser Lys Leu Val Asp Pro Lys Met Lys Leu Ser Thr Arg  
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 35 40 45  
 Trp Val Ile Thr Gly Asp Asn Arg Ser Pro Cys Asn Trp Thr Gly Ile  
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 Thr Cys His Ile Arg Lys Gly Ser Ser Leu Ala Val Thr Thr Ile Asp  
 65 70 75 80

Leu Ser Gly Tyr Asn Ile Ser Gly Gly Phe Pro Tyr Gly Phe Cys Arg  
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 Ile Arg Thr Leu Ile Asn Ile Thr Leu Ser Gln Asn Asn Leu Asn Gly  
 100 105 110  
 Thr Ile Asp Ser Ala Pro Leu Ser Leu Cys Ser Lys Leu Gln Asn Leu  
 115 120 125  
 Ile Leu Asn Gln Asn Asn Phe Ser Gly Lys Leu Pro Glu Phe Ser Pro  
 130 135 140  
 Glu Phe Arg Lys Leu Arg Val Leu Glu Leu Glu Ser Asn Leu Phe Thr  
 145 150 155 160  
 Gly Glu Ile Pro Gln Ser Tyr Gly Arg Leu Thr Ala Leu Gln Val Leu  
 165 170 175  
 Asn Leu Asn Gly Asn Pro Leu Ser Gly Ile Val Pro Ala Phe Leu Gly  
 180 185 190  
 Tyr Leu Thr Glu Leu Thr Arg Leu Asp Leu Ala Tyr Ile Ser Phe Asp  
 195 200 205  
 Pro Ser Pro Ile Pro Ser Thr Leu Gly Asn Leu Ser Asn Leu Thr Asp  
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 Leu Arg Leu Thr His Ser Asn Leu Val Gly Glu Ile Pro Asp Ser Ile  
 225 230 235 240  
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Tyr Arg Arg Lys Leu Gln Lys Ile Ile Thr Phe Ser Asn Gln Leu Ser  
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 Gly Glu Ile Pro Glu Ser Tyr Gly Asp Cys His Ser Leu Asn Tyr Ile  
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 Arg Met Ala Asp Asn Lys Leu Ser Gly Glu Val Pro Ala Arg Phe Trp  
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